

; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-613-137

Query Match 98.7%; Score 1092; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 7.8e-102;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 52
Db 24 GRLLSASDLDLRGGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 83

QY 53 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112
Db 84 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143

QY 113 SCGSEVCVMYHQPSAPAGIGGPFYMFQWDDRCNKNPFICKYSDEKPAVPSREAEGET 172
Db 144 SCGSEVCVMYHQPSAPAGIGGPFYMFQWDDRCNKNPFICKYSDEKPAVPSREAEGET 203

QY 173 ELTTPVLPEETOEDAKKTFKESREAAALNLAY 204
Db 204 ELTTPVLPEETOEDAKKTFKESREAAALNLAY 235

RESULT 20
US-09-907-942-137
; Sequence 137, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-942-137

Query Match 98.7%; Score 1092; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 7.8e-102;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 52
Db 24 GRLLSASDLDLRGGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 83

QY 53 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112
Db 84 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143

; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-204-137

Query Match 98.7%; Score 1092; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 7.8e-102;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEAAKEACRRDGGQLVSIES 52
Db 24 GRLLSASDLRLGGQPVCRGGTQPCYKVIYFHDTSRRLNFEAAKEACRRDGGQLVSIES 83

QY 53 EDEQKLEKFIENLLPSDGFNIGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112
Db 84 EDEQKLEKFIENLLPSDGFNIGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143

QY 113 SCGSEVCVMYHQPSAPAGIGGYPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGET 172
Db 144 SCGSEVCVMYHQPSAPAGIGGYPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGET 203

QY 173 ELTTPVLPEETQEEDAKKTFKESREAAINLAY 204
Db 204 ELTTPVLPEETQEEDAKKTFKESREAAINLAY 235

RESULT 23
US-09-904-820-137
; Sequence 137, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-820-137

Query Match 98.7%; Score 1092; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 7.8e-102;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEAAKEACRRDGGQLVSIES 52
Db 24 GRLLSASDLRLGGQPVCRGGTQPCYKVIYFHDTSRRLNFEAAKEACRRDGGQLVSIES 83

QY 53 EDEQKLEKFIENLLPSDGFNIGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112

Db 84 EDEQKLEKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143
QY 113 SCGSEVCVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGEET 172
Db 144 SCGSEVCVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGEET 203
QY 173 ELTTPVLPEETOEDAKKTFKESREAAINLAY 204
Db 204 ELTTPVLPEETOEDAKKTFKESREAAINLAY 235

RESULT 24
US-09-904-786-137
; Sequence 137, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,786
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/565,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-786-137

Query Match 98.7%; Score 1092; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 7.8e-102;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 GRLLS-----GQVCEGGTQPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSIES 52
Db 24 GRLLSASDLRLGGQPVCEGGTQPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSIES 83
QY 53 EDEQKLEKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112
Db 84 EDEQKLEKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143
QY 113 SCGSEVCVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGEET 172
Db 144 SCGSEVCVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGEET 203
QY 173 ELTTPVLPEETOEDAKKTFKESREAAINLAY 204

Db 204 ELTTPVLPEETOEDAKKTFKESREAAINLAY 235
RESULT 25
US-09-906-646-137
; Sequence 137, Application US/09906646
; Publication No. US20030039971A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,646
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05


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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-646-137

Query Match      98.7%; Score 1092; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 7.8e-102;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY      1 GRLLS-----GQPVCRGGTQRPCYKVIYFHDTSRRRLNFEEAKEACRRDGGQLVSIES 52
      |||||
Db      24 GRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRRLNFEEAKEACRRDGGQLVSIES 83

QY      53 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEP 112
      |||||
Db      84 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNYYVDEP 143

QY      113 SCGSEVCVVMYHQPSAPAGIGGPPYMFQWNDRCNMKNNFICKYSDEKPAVPSREAEGET 172
      |||||
Db      144 SCGSEVCVVMYHQPSAPAGIGGPPYMFQWNDRCNMKNNFICKYSDEKPAVPSREAEGET 203

QY      173 ELTTPVLPEETOEEADAKKTFKESREAAALNLAY 204
      |||||
Db      204 ELTTPVLPEETOEEADAKKTFKESREAAALNLAY 235
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Job time : 91.7224 secs

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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:48:35 ; Search time 25.0614 Seconds
(without alignments)
782.999 Million cell updates/sec

Title: US-09-887-855-2_COPY_24_227
Perfect score: 1106
Sequence: 1 GRLLSGQPVCRGGTQPCYK.....EEDAKTKESREAALNLAY 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	182	16.5	1456	1 A36563	mannose receptor p
2	178.5	16.1	1455	1 A48925	mannose receptor p
3	177	16.0	1268	2 S52781	neurocan - mouse
4	174.5	15.8	1643	2 T14274	versican precursor
5	174.5	15.8	3381	2 T42389	versican precursor
6	174	15.7	1257	2 S28764	neurocan precursor
7	174	15.7	2397	1 A55535	versican precursor
8	174	15.7	2409	1 A60979	versican precursor
9	171	15.5	3562	2 A47171	chondroitin sulfat
10	170.5	15.4	1479	2 T42710	mannose receptor,
11	158.5	14.3	1340	2 A39808	proteoglycan core
12	158.5	14.3	2327	2 T42630	aggrecan - bovine
13	158.5	14.3	2415	1 A39086	aggrecan precursor
14	154.5	14.0	612	2 B42755	E-selectin precurs
15	153.5	13.9	2124	2 A28452	proteoglycan core
16	152	13.7	912	2 A54423	brevican precursor
17	149.5	13.5	459	2 T24425	hypothetical prote
18	149	13.5	321	1 LNHUER	IgE Fc receptor II
19	148.5	13.4	330	2 T46256	brevican - human (
20	148	13.4	253	2 B89130	protein F52E1.2 [i
21	147.5	13.3	2132	1 A55182	aggrecan precursor
22	147	13.3	883	2 S57653	brevican precursor
23	146.5	13.2	162	1 LNRCL	lectin BRA3-1 prec
24	146	13.2	2109	1 I50421	aggrecan precursor
25	145.5	13.2	742	2 JC7595	scavenger receptor
26	145	13.1	883	2 S49126	brevican precursor
27	144.5	13.1	173	2 S10548	lectin - barnacle
28	144.5	13.1	372	2 S23936	L-selectin precurs
29	144.5	13.1	404	2 A46274	HIV gp120-binding

30	143.5	13.0	129	2 JC4329	coagulation factor
31	143.5	13.0	372	1 A32375	L-selectin precurs
32	143.5	13.0	463	2 T26655	hypothetical prote
33	142.5	12.9	131	2 JC5058	bitiscetin alpha c
34	142	12.8	1487	2 S48719	phospholipase-A(2)
35	141.5	12.8	331	1 LNMSE	IgE Fc receptor, I
36	140.5	12.7	162	1 LNRCL	lectin BRA3-2 prec
37	140	12.7	370	2 S22124	L-selectin precurs
38	139	12.6	248	1 LNHUPS	pulmonary surfacta
39	139	12.6	248	1 LNHUP6	pulmonary surfacta
40	139	12.6	248	1 LNHUP1	pulmonary surfacta
41	139	12.6	283	1 LNFHLS	lectin precursor -
42	138.5	12.5	152	2 JC4690	coagulation factor
43	138.5	12.5	202	2 JC4031	tetranectin precu
44	138	12.5	280	2 T29200	hypothetical prote
45	137.5	12.4	309	1 S34198	IgE Fc receptor II

ALIGNMENTS

RESULT 1

A36563

mannose receptor precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999

C;Accession: A36563; A60926; A44255; B44255; C44255; E44255; F44255; G44255; H44

R;Taylor, M.E.; Conary, J.T.; Lennartz, M.R.; Stahl, P.D.; Drickamer, K.

J. Biol. Chem. 265, 12156-12162, 1990

A;Title: Primary structure of the mannose receptor contains multiple motifs resembling c

A;Reference number: A36563; MUID:90324192; PMID:2373685

A;Accession: A36563

A;Molecule type: mRNA

A;Residues: 1-1456 <TAY>

A;Cross-references: GB:J05550; NID:G188675; PIDN:AAA59868.1; PID:G188676

A;Note: parts of this sequence, including the amino end of the mature protein, were conf

R;Ezekowitz, R.A.B.; Sastry, K.; Bailly, P.; Warner, A.

J. Exp. Med. 172, 1785-1794, 1990

A;Title: Molecular characterization of the human macrophage mannose receptor: demonstrat

A;Reference number: A60926; MUID:91079783; PMID:2258707

A;Accession: A60926

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1333, T', 1335-1456 <EZE>

A;Cross-references: GB:X55635

A;Note: translation of the nucleotide sequence is incomplete

A;Note: in the authors' translation additional residues Pro-Glu-Ile are shown after 497-

R;Kim, S.J.; Ruiz, N.; Bezouska, K.; Drickamer, K.

Genomics 14, 721-727, 1992

A;Title: Organization of the gene encoding the human macrophage mannose receptor (MRC1).

A;Reference number: A44255; MUID:93052405; PMID:1294118

A;Accession: A44255

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: DNA

A;Residues: 155-233, 'KSAL', 238-283; 346-428; 492-569; 631-714, 716-719; 783-820, 'N', 822-865; '

A;Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421, NCBIP:118428,

C;Genetics:

A;Gene: GDB:MRC1

A;Cross-references: GDB:133759; OMIM:153618

A;Map position: 10p13-10p13

C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re

C;Keywords: duplication; lectin; tandem repeat; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;168-209/Domain: fibronectin type II repeat homology <2F1>

F;223-340/Domain: C-type lectin homology <LCH1>

F;362-486/Domain: C-type lectin homology <LCH2>

F;945-1079/Domain: C-type lectin homology <LCH3>

Query Match 16.5%; Score 182; DB 1; Length 1456;

Best Local Similarity 25.5%; Pred. No. 8.8e-08;

Matches 52; Conservative 37; Mismatches 61; Indels 54; Gaps 8;

QY 19 YKVIYFHDTSRRLNFEAEKACRRDGGQLVSIIESEDEKLIKFIENLLPSDGDWIGLR 78

Db 807 YKDYQYFSKEKETMDNARAFCKRNFGLDLSIQSESEKFLWKYV-NRNDASAYFIGLL 865

QY 79 RREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGS--EVCVVMYHQPSPAGIGGPY 136

Db 866 ISLDKK-----FAWMDGSKVDYVSWATGEPNFANEDENCVTMY-----SNSGF---- 908

QY 137 MFQWDDRCNMKNFNICKYSDEK----PAVPSREABGEETEELTTPVLPEETQE----- 185

Db 909 ---WINDINGYPNAFICQPHNSINATTVM-----TMPSPVSGCKEGWNFYSN 954

QY 186 -----EDAKTFKESREAAAL 200

Db 955 KCFKIFGFMEBERKNWQEARACI 978

RESULT 2

A48925

mannose receptor precursor, macrophage - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A48925; S21320; PC2245

R;Harris, N.; Super, M.; Rits, M.; Chang, G.; Ezekowitz, R.A.

Blood 80, 2363-2373, 1992

A;Title: Characterization of the murine macrophage mannose receptor: demonstration that

A;Reference number: A48925; MUID:93043353; PMID:1421407

A;Accession: A48925

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-1455 <HAR>

A;Experimental source: peritoneal macrophage

A;Note: sequence extracted from NCBI backbone (NCBIP:118733)

R;Harris, N.; Super, M.; Rits, M.; Chang, G.; Ezekowitz, R.B.

submitted to the EMBL Data Library, April 1992

A;Description: Characterization of the murine macrophage mannose receptor: Demonstration

on.

A;Reference number: S21320

A;Accession: S21320

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-302,'W',303-1117,'B',1119-1455 <HA2>

A;Cross-references: EMBL:Z11974; NID:G52997; PIDN:CAA78028.1; PID:G52998

R;Harris, N.; Peters, L.L.; Elcher, E.M.; Rits, M.; Rasperry, D.; Eichbaum, Q.G.; Super

Biochem. Biophys. Res. Commun. 198, 682-692, 1994

A;Title: The exon-intron structure and chromosomal localization of the mouse macrophage

A;Reference number: PC2245; MUID:94128116; PMID:8297379

A;Accession: PC2245

A;Molecule type: mRNA

A;Residues: 35-105 <HA3>

C;Genetics:

A;Gene: Mrc1

A;Map position: 2

C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re

C;Keywords: membrane protein; receptor

F;168-209/Domain: fibronectin type II repeat homology <2F9>

F;361-485/Domain: C-type lectin homology <LCH1>

F;943-1077/Domain: C-type lectin homology <LCH2>

Query Match 16.1%; Score 178.5; DB 1; Length 1455;

Best Local Similarity 25.9%; Pred. No. 1.8e-07;

Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;

QY 19 YKVIYFHDTSRRLNFEAEKACRRDGGQLVSISEDEQKLIKFIENLLPSDGFWIGLR 78

Db 806 YKDYQYFSKEKETMDNARFCKKNFGDLATIKSESEKFLWKYI-NKNGGQSPYFIGML 864

QY 79 RREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGS--EVCVVMYHQPSPAGIGGPY 136

Db 865 ISMDKK-----FIWMDGSKVDVAVATGEPNFANDDENCVTMY-----TNSGF---- 907

QY 137 MFQWDDRCNMKNFNICK---YSDEKPAVPSREABGEETEELTTPVLPEETQE----- 185

QY 186 -----EDAKTFKESREAAALN 202

Db 954 CFKIFGFANEKKSQDARQACKGL 978

RESULT 3

S52781

neurocan - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000

C;Accession: S52781

R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.

submitted to the EMBL Data Library, February 1995

A;Description: Amino acid sequence of mouse neurocan and their different ex

A;Reference number: S52781

A;Accession: S52781

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1268 <RAU>

A;Cross-references: EMBL:X84727; NID:G758629; PIDN:CAA59216.1; PID:G758630

C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF

F;176-253/Domain: link protein repeat homology <LNK1>

F;274-355/Domain: link protein repeat homology <LNK2>

F;964-995/Domain: EGF homology <EGF>

F;1040-1160/Domain: C-type lectin homology <LCH>

F;1167-1223/Domain: complement factor H repeat homology <FHD>

Query Match 16.0%; Score 177; DB 2; Length 1268;

Best Local Similarity 31.5%; Pred. No. 2.1e-07;

Matches 45; Conservative 17; Mismatches 49; Indels 32; Gaps 6;

QY 15 QRPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSISEDEQKLIKFIENLLPSDGF 74

Db 1048 QGHCYR--YF--AHRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW 1096

QY 75 IGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS---CGSEVCVVMYHQPSPAG 131

Db 1097 IGLNDRITVERD-----FQWTDNTGLQYENWREKQPDNFFAGGEDCVVMVAHESG--- 1145

QY 132 IGGPYMFQWDDRCNMKNFNICK 154

Db 1146 -----RWNDVPCNVNLPYVCK 1161

RESULT 4

T14274

versican precursor, splice form V2 - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000

C;Accession: T14274

R;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.

J. Biol. Chem. 273, 15758-15764, 1998

A;Title: Versican V2 is a major extracellular matrix component of the mature bovine brain

A;Reference number: Z17954; MUID:98288320; PMID:9624174

A;Accession: T14274

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1643 <SCH>

A;Cross-references: EMBL:AF060458; NID:G3253303; PID:G3253304; PIDN:AAC24360.1

A;Experimental source: brain

C;Keywords: glycoprotein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-1643/Product: versican, splice form V2 #status predicted <MAT>

F;57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 15.8%; Score 174.5; DB 2; Length 1643;

Best Local Similarity 25.5%; Pred. No. 4.7e-07;

Matches 59; Conservative 26; Mismatches 71; Indels 75; Gaps 11;

QY 15 QRPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSISEDEQKLIKFIENLLPSDGF- 73

Db 1424 CCOCYK--YF--AHRTWDAAFRFCRIQGAHLTSLSHEEOMFVNRV-----GHDYQ 1471

RESULT 8
A60979
versican precursor - human
N;Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
N;Contains: glial hyaluronate-binding protein
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 19-Jan-2001
C;Accession: S06014; S43921; A60979; A30358; A29348; A45131; I54179
R;Zimmermann, D.R.; Ruoslahti, E.
EMBO J. 8, 2975-2981, 1989
A;Title: Multiple domains of the large fibroblast proteoglycan, versican.
A;Reference number: S06014; MUID:90059882; PMID:2583089
A;Accession: S06014
A;Molecule type: mRNA
A;Residues: 1-2409 <ZIM>
A;Cross-references: GB:X15998; NID:G37662; PIDN:CAA34128.1; PID:G37663
R;Yao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
A;Title: Identification of the proteoglycan versican in aorta and smooth muscle cells by
A;Reference number: S43921; MUID:95005762; PMID:7921538
A;Accession: S43921
A;Molecule type: mRNA
A;Residues: 208-440;1094-1385;1910-2246 <YAO>
R;Bignami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
Brain Res. Bull. 22, 67-70, 1989
A;Title: Structural similarity of hyaluronate binding proteins in brain and cartilage.
A;Reference number: A60979; MUID:89229983; PMID:2469524
A;Accession: A60979
A;Molecule type: protein
A;Residues: 171-210;289-303 <BIG>
R;Perides, G.; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
J. Biol. Chem. 264, 5981-5987, 1989
A;Title: Isolation and partial characterization of a glial hyaluronate-binding protein.
A;Reference number: A30358; MUID:89174663; PMID:2466833
A;Accession: A30358
A;Molecule type: protein
A;Residues: 24-50;80-87, 'D', 89-119;128-155;167-218;229-259, 'TR';261-268;277-283, 'G', 285-
R;Krusius, T.; Gehlsen, K.R.; Ruoslahti, E.
J. Biol. Chem. 262, 13120-13125, 1987
A;Title: A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like
A;Reference number: A29348; MUID:88007514; PMID:2820964
A;Accession: A29348
A;Molecule type: mRNA
A;Residues: 1725, 'V', 1727-2409 <KRU>
A;Cross-references: GB:J02814
R;Perides, G.; Rahemtulla, F.; Lane, W.S.; Asher, R.A.; Bignami, A.
J. Biol. Chem. 267, 23883-23887, 1992
A;Title: Isolation of a large aggregating proteoglycan from human brain.
A;Reference number: A45131; MUID:93054750; PMID:1429726
A;Contents: brain
A;Accession: A45131
A;Molecule type: protein
A;Residues: 21-22, 'X', 24-37 <PE2>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118884)
R;Iozzo, R.V.; Naso, M.F.; Cannizzaro, L.A.; Wasmuth, J.J.; McPherson, J.D.
Genomics 14, 845-851, 1992
A;Title: Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chro
A;Reference number: I54179; MUID:93122792; PMID:1478664
A;Accession: I54179
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 251-347 <RES>
A;Cross-references: GB:S52488; NID:G263313; PIDN:AAB24878.1; PID:G263314
C;Genetics:
A;Gene: GDB:CSPG2
A;Cross-references: GDB:127873; OMIM:118661
A;Map position: 5q12-5q14
C;Superfamily: versican; C-type lectin homology; complement factor H repeat homology; EG
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-2409/Product: proteoglycan 24K core protein #status predicted <MAT>
F;167-244/Domain: link protein repeat homology <LNK1>

F;265-346/Domain: link protein repeat homology <LNK2>
F;559-1654/Domain: chondroitin sulfate attachment #status predicted <GAG>
F;2106-2137/Domain: EGF homology <EG1>
F;2144-2175/Domain: EGF homology <EG2>
F;2182-2302/Domain: C-type lectin homology <LCH>
F;2309-2365/Domain: complement factor H repeat homology <FHD>
Query Match 15.7%; Score 174; DB 1; Length 2409;
Best Local Similarity 28.5%; Pred. No. 8.1e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
Qy 15 QRPCKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLIKFIENLLPSDGD- 73
Db 2190 QGQCYK--YF---AHRRTWDAARECRLOGAHLTSILSHEEQMFVNRV-----GHDIYQ 2237
Qy 74 WIGLRRREKQNSSTACQDLYAWTDGSIQFRNWIYVDEP-----SCGSEVCVVMYHQPSAP 129
Db 2238 WIGL-----NDKMFEDHDFRWTGSLQYENWRPNQPDSPFSAGEDCVVLIWHENG-- 2287
Qy 130 AGIGGPMFQWDDRCNMKNFNICKYS----DEKPAVPSREAEGE 170
Db 2288 -----QWNDVPCNYHLTYTCKKGTACGQPPVVENAKTFGK 2323
RESULT 9
A47171
chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text change 21-Jul-2000
C;Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during
A;Reference number: A47171; MUID:93300846; PMID:8314802
A;Accession: A47171
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-3562 <SHI>
A;Cross-references: GB:D13542; NID:G391643; PIDN:BAA02742.1; PID:G391644
A;Experimental source: stage 22-23 developing limb buds
A;Note: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457)
C;Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin
F;166-243/Domain: link protein repeat homology <LNK1>
F;264-345/Domain: link protein repeat homology <LNK2>
F;3258-3289/Domain: EGF homology <EGF1>
F;3296-3327/Domain: EGF homology <EGF>
F;3334-3454/Domain: C-type lectin homology <LCH>
F;3461-3517/Domain: complement factor H repeat homology <FHD>
Query Match 15.5%; Score 171; DB 2; Length 3562;
Best Local Similarity 28.5%; Pred. No. 2.4e-06;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
Qy 15 QRPCKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLIKFIENLLPSDGD- 73
Db 3342 QGQCYK--YF---AHRRTWDTAARECRLOGAHLTSILSHEEQVFNRI-----GHDIYQ 3389
Qy 74 WIGLRRREKQNSSTACQDLYAWTDGSIQFRNWIYVDEP-----SCGSEVCVVMYHQPSAP 129
Db 3390 WIGL-----NDKMFEDHDFRWTGSLQYENWRPNQPDSPFSAGEDCVVLIWHENG-- 3439
Qy 130 AGIGGPMFQWDDRCNMKNFNICKYS----DEKPAVPSREAEGE 170
Db 3440 -----QWNDVPCNYHLTYTCKKGTACGQPPVVENAKTFGK 3475
RESULT 10
T42710
mannose receptor, macrophage - mouse
N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 09-Jun-2000

C;Accession: T42710
R;Wu, K.; Yuan, J.; Lasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996
A;Title: Characterization of a novel member of the macrophage mannose receptor type C le
A;Reference number: Z22235; MUID:96355501; PMID:8702911
A;Accession: T42710
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1479 <WUK>
A;Cross-references: EMBL:U56734; NID:gl336073; PID:gl336074; PIDN:AAC52729.1
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C;Keywords: membrane protein; receptor
F;186-227/Domain: fibronectin type II repeat homology <2FR>

Query Match 15.4%; Score 170.5; DB 2; Length 1479;
Best Local Similarity 31.4%; Pred. No. 9.4e-07;
Matches 48; Conservative 22; Mismatches 48; Indels 35; Gaps 7;

Qy 5 SQPVCRCGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI ESEDEQKLI EKFI 64
Db 384 SWQPF-----QGH CYRL-----QA EKRSWQESKRACLRGGDL LSIHSM AELEF ITKQIK 433

Qy 65 NLLPSDGD F WIGLRRRREEKQSNSTACQDLYAWTDGSI S QFRN WYVDEPS---CGSEV CVW 121
Db 434 QEVE---ELWIGL-----NDLKLQMNFEWSDGSLVSFTWHHPFPENFRDLSLDCVT 482

Qy 122 MYHQPSAPAGIGGPPYMFQWNDRCNMKNFNICK 154
Db 483 IW----GPEG-----RWNDSPCNQSLPSICK 504

RESULT 11
A39808
proteoglycan core protein, cartilage - bovine (fragments)
N;Alternate names: aggrecan; aggregating cartilage proteoglycan
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Mar-1992 #sequence revision 23-Mar-1995 #text change 13-Aug-1999
C;Accession: A34234; A27752; A39808; A27751; E29164; B27751; C27751; E27751; F27
R;Antonsson, P.; Heinegard, D.; Oldberg, A.
J. Biol. Chem. 264, 16170-16173, 1989
A;Title: The keratan sulfate-enriched region of bovine cartilage proteoglycan consists o
A;Reference number: A34234; MUID:89380219; PMID:2528543
A;Accession: A34234
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 128-621 <ANT>
A;Cross-references: GB:J05028
R;Oldberg, A.; Antonsson, P.; Heinegard, D.
Biochem. J. 243, 255-259, 1987
A;Title: The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a
A;Reference number: A27752; MUID:87270630; PMID:3111460
A;Accession: A27752
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 622-1340 <OLD>
R;Sandy, J.D.; Boynton, R.E.; Flannery, C.R.
J. Biol. Chem. 266, 8198-8205, 1991
A;Title: Analysis of the catabolism of aggrecan in cartilage explants by quantitation of
A;Reference number: A39808; MUID:91217051; PMID:2022637
A;Accession: A39808
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28;59-82;131-137,'QSET',142-149;196-207;226-249;1137-1143;1252-1267;1274-1
R;Perin, J.P.; Bonnet, F.; Jolles, P.
FEBS Lett. 206, 73-77, 1986
A;Title: Structural relationship between link proteins and proteoglycan monomers.
A;Reference number: A27751; MUID:87005253; PMID:3530809
A;Accession: A27751
A;Molecule type: protein
A;Residues: 29-58;74-130;174-175,'A',177-204;208-225 <PER>
R;Perin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.
FEBS Lett. 176, 37-42, 1984
A;Title: Sequence data concerning the protein core of the cartilage proteoglycan monomer

A;Reference number: A91327; MUID:85027710; PMID:6489519
A;Accession: E29164
A;Molecule type: protein
A;Residues: 1230-1249 <PE2>
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: glycoprotein
F;8-28/Domain: link protein repeat homology (fragment) <LNK1>
F;29-58/Domain: link protein repeat homology (fragment) <LNK2>
F;80-146/Domain: link protein repeat homology (fragments) <LNK3>
F;167-248/Domain: link protein repeat homology <LNK4>
F;1130-1250/Domain: C-type lectin homology <LCH>
F;1257-1313/Domain: complement factor H repeat homology <PHD>

Query Match 14.3%; Score 158.5; DB 2; Length 1340;
Best Local Similarity 26.8%; Pred. No. 9.7e-06;
Matches 48; Conservative 29; Mismatches 59; Indels 43; Gaps 10;

Qy 7 QPVCRCGG---TORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI ESEDEQKLI EKFI 63
Db 1127 QKLCEEGWTKFQGH CYR--HFPD---RATWVDAESQCRKQOSHLS SIVTPEEQ----EFV 1177

Qy 64 ENLLPSDGD F WIGLRRRREEKQSNSTACQDLYAWTDGSI S QFRN WYVDEP---SCGSEV 118
Db 1178 NN---NAQDYQWIGL-----NDKTIEGDFRWS DGHSLQFENWRPNQPDNFFATGEDC 1226

Qy 119 CVVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFNICKYS----DEKPAVPSREAEGEETE 173
Db 1227 VVMIWHEKG-----EWNDVPCNYQLPFTCKKGT VACGPPVVEHARIFGQKXD 1274

RESULT 12
T42630
aggrecan - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T42630
R;Hering, T.M.; Kollar, J.; Huynh, T.D.
submitted to the EMBL Data Library, September 1996
A;Description: Complete coding sequence of bovine aggrecan: comparative structural analy
A;Reference number: Z22182
A;Accession: T42630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2327 <HER>
A;Cross-references: EMBL:U76615; NID:gl730259; PID:gl730260; PIDN:AAB38524.1
A;Experimental source: articular chondrocytes
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycoprot

Query Match 14.3%; Score 158.5; DB 2; Length 2327;
Best Local Similarity 26.8%; Pred. No. 1.8e-05;
Matches 48; Conservative 29; Mismatches 59; Indels 43; Gaps 10;

Qy 7 QPVCRCGG---TORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI ESEDEQKLI EKFI 63
Db 2114 QKLCEEGWTKFQGH CYR--HFPD---RATWVDAESQCRKQOSHLS SIVTPEEQ----EFV 2164

Qy 64 ENLLPSDGD F WIGLRRRREEKQSNSTACQDLYAWTDGSI S QFRN WYVDEP---SCGSEV 118
Db 2165 NN---NAQDYQWIGL-----NDKTIEGDFRWS DGHSLQFENWRPNQPDNFFATGEDC 2213

Qy 119 CVVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFNICKYS----DEKPAVPSREAEGEETE 173
Db 2214 VVMIWHEKG-----EWNDVPCNYQLPFTCKKGT VACGPPVVEHARIFGQKXD 2261

RESULT 13
A39086
aggrecan precursor, cartilage long splice form [validated] - human
N;Alternate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan; p
N;Contains: aggrecan cartilage short splice form
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000

C;Accession: A39086; S50206; A43919; S46659; S66389; S68646; S62786; A34226; B43919; C43
R;Doerge, K.J.; Sasaki, M.; Kimura, T.; Yamada, Y.
J. Biol. Chem. 266, 894-902, 1991
A;Title: Complete coding sequence and deduced primary structure of the human cartilage
A;Reference number: A39086; MUID:91093289; PMID:1985970
A;Accession: A39086
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2162;2201-2329,'A',2392-2415 <DOE>
A;Cross-references: GB:M55172; NID:g178258; PIDN:AAA62824.1; PID:g178259
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Accession: S50206
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 350-497 <GLU>
A;Cross-references: EMBL:X80278; NID:g516295
A;Note: this translation is not annotated in GenBank entry HSAGGREC, release 113.0
R;Sandy, J.D.; Flannery, C.R.; Neame, P.J.; Lohmander, L.S.
J. Clin. Invest. 89, 1512-1516, 1992
A;Title: The structure of aggrecan fragments in human synovial fluid. Evidence for the
domain.
A;Reference number: A43919; MUID:92235266; PMID:1569188
A;Accession: A43919
A;Molecule type: protein
A;Residues: 361-370,'X',372-373;393-399,'X',401-407,'X',409 <SAN>
A;Cross-references: PIDN:AAB22079.1; PID:g248844; PIDN:AAB22077.1; PID:g248842; PIDN:AAB
A;Experimental source: synovial fluid
A;Note: sequences modified after extraction from NCBI backbone
R;Barry, F.P.; Neame, P.J.; Sasse, J.; Pearson, D.
Matrix Biol. 14, 323-328, 1994
A;Title: Length variation in the keratan sulfate domain of mammalian aggrecan.
A;Reference number: I46998; MUID:95128522; PMID:7827755
A;Accession: S46659
A;Molecule type: DNA
A;Residues: 764-765,'A',767-846,'V',848-862,'X',864 <BAR>
A;Cross-references: EMBL:S74659; NID:g807127; PIDN:AAC60643.1; PID:g807128
A;Note: the authors translated the codon GAA for residue 803 as Ala and Cyt for residue
R;Illic, M.Z.; Mok, M.T.; Williamson, O.D.; Campbell, M.A.; Hughes, C.E.; Handley, C.J.
Arch. Biochem. Biophys. 322, 22-30, 1995
A;Title: Catabolism of aggrecan by explant cultures of human articular cartilage in the
A;Reference number: S66389; MUID:96004775; PMID:7574678
A;Accession: S66389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 17-23;24,'X',26-27;393-401;402-403 <ILI>
R;Fosang, A.J.; Last, K.; Knaeuper, V.; Murphy, G.; Neame, P.J.
FEBS Lett. 380, 17-20, 1996
A;Title: Degradation of cartilage aggrecan by collagenase-3 (NMP-13).
A;Reference number: S68646; MUID:96181659; PMID:8603731
A;Accession: S68646
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'V',404-405,'XX' <FOS>
R;Dudhia, J.; Davidson, C.M.; Wells, T.M.; Vynios, D.H.; Hardingham, T.E.; Bayliss, M.T.
Biochem. J. 313, 933-940, 1996
A;Title: Age-related changes in the content of the C-terminal region of aggrecan in huma
A;Reference number: S62786; MUID:96190740; PMID:8611178
A;Accession: S62786
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1778-1927,'A',1929-1963,'V',1965-2162,2201-2415 <DUD>
A;Cross-references: EMBL:X17406; NID:g30248; PIDN:CAA35463.1; PID:g30249
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1990
R;Baldwin, C.T.; Reginato, A.M.; Prockop, D.J.
J. Biol. Chem. 264, 15747-15750, 1989
A;Title: A new epidermal growth factor-like domain in the human core protein for the lar
A;Reference number: A34226; MUID:89380154; PMID:2789216
A;Accession: A34226
A;Molecule type: mRNA
A;Residues: 1936-1963,'V',1965-2069,'A',2071-2415 <BAL>

A;Cross-references: GB:J05062; NID:g1811167; PIDN:AAA35726.1; PID:g1811168
C;Genetics:
A;Gene: GDB:AGC1; CSPG1; CSPGCP; MSK16
A;Cross-references: GDB:127479; OMIM:155760
A;Map position: 15q26-15q26
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF
C;Keywords: alternative splicing; cartilage; chondroitin sulfate proteoglycan; extracellu
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-2415/Product: aggrecan cartilage long splice form #status predicted <MATL>
F;20-2162,2201-2415/Product: aggrecan cartilage short splice form #status predicted <MATN
F;20-2162,2201-2329,'A',2392-2415/Product: aggrecan short splice form #status predicted <
F;44-135/Domain: immunoglobulin homology <IMM>
F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;495-572/Domain: link protein repeat homology <LNK3>
F;593-673/Domain: link protein repeat homology <LNK4>
F;677-861/Domain: keratan sulfate attachment #status predicted <KSA>
F;864-1510/Domain: chondroitin sulfate attachment #status predicted <CS1>
F;1511-2162/Domain: chondroitin sulfate attachment #status predicted <CS2>
F;2168-2198/Domain: EGF homology <EGF>
F;2205-2325/Domain: C-type lectin homology <LCH>
F;2332-2388/Domain: complement factor H repeat homology <FHD>
F;126,239,333,387,434,602,657,737,1898/Binding site: carbohydrate (Asn) (covalent) #statu
F;371,376/Binding site: keratan sulfate (Thr) (covalent) #status predicted

Query Match 14.3%; Score 158.5; DB 1; Length 2415;
Best Local Similarity 29.1%; Pred. No. 1.9e-05;
Matches 52; Conservative 22; Mismatches 62; Indels 43; Gaps 11;
QY 7'QPVCRRG---TORPCYKVIYFHDTSRRLLNFEEAKERRDGGQLVSISEDEQKLEKFI 63
Db 2202 QEVCEEGWNKYQGHCYR--HFPD---RETWVDAERRCRREQQSHLSSIVTPEEQ----EFV 2252
QY 64 ENLLPSDGDGFWIGLRREKQSNSTACQDLVATWTDGSIQFRNWWYVDEPS---CGSEVC 119
Db 2253 NN---NAQDYQWIGL-----NDRITIEGDFRWDGHPMQFENWRPNQPDNFFAAGDC 2301
QY 120 VVM-YHQPSAPAGIGGPGYMFQWDDRCNMKNFKICKYS---DEKPAVPSREAEGEETE 173
Db 2302 VVMIWHEKG-----EWNDVPCNYHLPTCKKGTACGEPVVEHARTFGQKXD 2349
RESULT 14
B42755
E-selectin precursor - mouse
N;Alternate names: endothelial leukocyte adhesion molecule 1 (ELAM-1)
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 31-Dec-2000 #text_change 02-Aug-2002
C;Accession: S23174; B42755
R;Becker-Andre, M.; van Huijsduijnen, R.H.; Losberger, C.; Whelan, J.; Delamarter, J.F.
Eur. J. Biochem. 206, 401-411, 1992
A;Title: Murine endothelial leukocyte-adhesion molecule 1 is a close structural and funct
A;Reference number: S23174; MUID:92283265; PMID:1375914
A;Accession: S23174
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-612 <BEC>
A;Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015
R;Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A;Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-selectin
A;Reference number: A42755; MUID:92340571; PMID:1378846
A;Accession: B42755
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 'MKATAGV',1-389;391-612 <WEL>
A;Cross-references: GB:M87862; NID:g193107
A;Experimental source: endothelial cells
A;Note: sequence extracted from NCBI backbone (NCBIP:109470)
A;Note: the sequence in GenBank entry MUSESELEC, release 117.0, (PIDN:AAA37577.1; PID:g19
A;Note: it is uncertain whether the initiator is Met-1 or the AUG codon preceding that
C;Superfamily: P-selectin; C-type lectin homology; complement factor H repeat homology; H
C;Keywords: glycoprotein; transmembrane protein


```
F;126,239,333,387,611,667,1842/Binding site: carbohydrate (Asn) (covalent) #status predicted
```

```
Query Match      13.9%; Score 153.5; DB 2; Length 2124;  
Best Local Similarity 26.3%; Pred. No. 4.6e-05;  
Matches 47; Conservative 27; Mismatches 62; Indels 43; Gaps 9;
```

QY 7 QPVCRRGG---TQRPCVKVIYFHDTSRRLNFEEAKEACRRDGGQLVSISEDEQKLIETFI 63
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1911 QEQCIEGWTKFQGHCHYR--HFDP---RETWVDAAERCRREQSHLSSIVTPPEEQEFVNKNA 1965
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 64 ENLLPSDGDF-WIGLRREEKQSNTACODLYAWTDGSISQFRNWWYVDEP----SCGSEV 118
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1966 Q-----DYQWIGL-----NDRTIEGDFRWSHGSLQFEKWRPNQPDNFFATGEDC 2010
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 119 CVVMYHQPSAPAGIGPYMFQWNDDRCNMKNFICKYS----DEKPAVPSPREAEGETE 173
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 2011 VVMIIWHERG-----EWNDRVPCNYQLPFTCKKGTVACGEPPAVEHARTLGQKXD 2058
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 16
A54423
brevican precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 21-Jan-2000
C;Accession: A54423; S41914
R;Yamada, H.; Watanabe, K.; Shimonaka, M.; Yamaguchi, Y.
J. Biol. Chem. 269, 10119-10126, 1994
A;Title: Molecular cloning of brevican, a novel brain proteoglycan of the aggrecan/versican family
A;Reference number: A54423; MUID:94193597; PMID:8144512
A;Accession: A54423
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-912 <YAM>
A;Cross-references: GB:X75887; NID:G452820; PIDN:CAA53481.1; PID:G452821
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG-F50-139/Domain: immunoglobulin homology <IMM>
F:174-251/Domain: link protein repeat homology <LNK1>
F:272-353/Domain: link protein repeat homology <LNK2>
F:551-682/Domain: EGF homology <EGF>
F:689-809/Domain: C-type lectin homology <LCH>
F:816-872/Domain: complement factor H repeat homology <PHD>

Query Match 13.7%; Score 152; DB 2; Length 912;
Best Local Similarity 28.8%; Pred. No. 2.3e-05;
Matches 47; Conservative 17; Mismatches 61; Indels 38; Gaps 8;

QY 15 QRPCVKVIYFHDTSRRLNFEEAKEACRRDGGQLVSISEDEQKLIETFIENLLPSDGDWF 74
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 697 QGACYK----HFSARR-SWEAEAKCRMVGAHLASISTPPEQDFNNRYEQ-----W 745
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 75 IGLRRREEKQSNTACODLYAWTDGSISQFRNWWYVDEPS---CGSEVCVVM-YHQPSAPA 130
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 746 IGL-----NDRTIEGDFLWSDGVPLLYENWNPQGPDSYFLSGENCVVMMVWHDAQ--- 794
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 131 GIGGPYNFQWNDDRCNMKNFICKYS----DEKPAVPSPREAEG 169
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 795 -----QWSDVPCNYHLSYTCKMGLVSCGPPPELPALAEVFG 829
 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 17
T24425
hypothetical protein T04A8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24425
R;Palmer, S.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19889
A;Accession: T24425
A>Status: preliminary; translated from GB/EMBL/DDBBJ
A:Molecule type: DNA
A;Residues: 1-459 <WIL>
A;Cross-references: EMBL:T235663; PIDN:CAA84726.1; GSPDB:GN00021; CESP:T04A8.3


```

A,Molecule type: DNA
A,Residues: 1-253 <STO>
A,Cross-references: GB:chr_V; PIDN:AAE37037.1; PID:gl086809; GSPDB:GN00023; CESP:F52E1.2
C,Genetics:
A:Gene: F52E1.2
A,Map position: 5

      Query Match      13.4%; Score 148; DB 2; Length 253;
      Best Local Similarity 29.2%; Pred. No. 1.2e-05;
      Matches 49; Conservative 24; Mismatches 57; Indels 38; Gaps 10;

QY 10 CRGG-----TQPCYKV-IYFHDTSRRLLNPEE-----AKEACRRDGGQLVSIES 52
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 96 CPGGCPTGWQYLNKCYKVLIIHFHCLSLKVLQKFDAAVTVAGATSACAAQGAELVTIDS 155

QY 53 EDEQKLIIEKFIEIEN--LLPSDGDGFWIGLRRREEKQSNSTACDLYAWTDGSIQFRNWYVD 110
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 156 FDENDALRKAFDTNALVDETKETWIGLK-----SLSGAWQ----WADGSSATYTNWAPS 205

QY 111 EPSCGSEVCVVMYHQPSPAGIGGPFYMFQ---WNDDRCNMKN-NFICK 154
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 206 OPS-SNGLCVOMITDLSLNA-----TYKYORGGWKTYGCGKTSASYICE 248

```

RESULT 21
A55182
aggrecan precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 21-Jan-2000
C/Accession: A55182; S55329; S50207; S51355; I78532; I58123
R/Walcz, E.; Deak, F.; Erhardt, P.; Coulter, S.N.; Fueioep, C.; Horvath, P.; Doege, K.J.
Genomics 22, 364-371, 1994
A/Title: Complete coding sequence, deduced primary structure, chromosomal localization,
A/Reference number: A55182; MUID:95104847; PMID:7806222
A/Accession: A55182
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-2132 <WAL>
A/Cross-references: GB:L07049; NID:G678541; PIDN:AAC37670.1; PID:gl91772
R/Watanabe, H.; Gao, L.; Sugiyama, S.; Doege, K.; Kimata, K.; Yamada, Y.
Biochem. J. 308, 433-440, 1995
A/Title: Mouse aggrecan, a large cartilage proteoglycan: protein sequence, gene structure
A/Reference number: S55329; MUID:95289972; PMID:7772024

A;Title: Mouse aggrecan, a large cartilage proteoglycan: Gene structure, sequence, and expression; PMID:7772024
A;Reference number: S55329; MUID:95289972; PMID:7772024
A;Accession: S55329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-567,'G',569-1728,'I',1730-2132 <WAT1>
A;Cross-references: GB:U22901; NID:G886014
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Accession: S50207
A;Molecule type: mRNA
A;Residues: 350-481,'R',483-506 <GLU1>
A;Cross-references: EMBL:X80279; NID:G673432
R;Glumoff, V.
Submitted to the EMBL Data Library, July 1994
A;Reference number: S51355

A;Accession: S51355
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 350-383, 'CPVMSQRERPWAA' <GLU2>
A;Cross-references: EMBL:X80279
R;Watanabe, H.; Kimata, K.; Line, S.; Strong, D.; Gao, L.Y.; Kozak, C.A.; Yamada, Y.
Nature Genet. 7, 154-157, 1994
A;Title: Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in the aggrecan gene
A;Reference number: I58123; MUID:95004579; PMID:7920633
A;Accession: I78532
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 211-326 <WAT2>
A;Cross-references: GB:S73722; NID:g765215; PIDN:AAB32160.1; PID:g765216

A;Accession: I58123
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 211-240, 'MCTASLRRWRVRSFMRHPQRNPSRRQPTS', 'AGGWHAMPQASSTWPGRAVWTC AALAGW', 'R
A;Cross-references: GB:S73720; NID:G765211; PIDN:AAB32159.1; PID:G765212
C;Genetics:
A;Map position: 7
A;Introns: 253/1
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC
C;Keywords: cartilage; extracellular matrix
F;1-19/Domain: signal sequence #status predicted <SIG>
F;44-135/Domain: immunoglobulin homology <IMM>
F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;504-581/Domain: link protein repeat homology <LNK3>
F;602-683/Domain: link protein repeat homology <LNK4>
F;1922-2042/Domain: C-type lectin homology <LCH>
F;2049-2105/Domain: complement factor H repeat homology <FHD>

Query Match 13.3%; Score 147.5; DB 1; Length 2132;
Best Local Similarity 24.7%; Pred. No. 0.00016;
Matches 45; Conservative 30; Mismatches 64; Indels 43; Gaps 9;

Qy 4 LSCQPVCRGG---TQPCVKVIYFHDTSRRLLNFEEAKEACRRDGGQLVSISEDEQKLI 60
Db 1916 VADQEQCEEGWTKFQGHYR--HFPD---RETWDAERRCREQQSHLSSIVTPPEEQEFVN 1970

Qy 61 KFIENLLPSDGDGF-WIGLRRREKQSNSTACQDLVAWTDGSGISQFRNYYVDEP----SCG 115
Db 1971 KNAQ-----DYQWIGL-----NDRTIEGDFRWSGDGHSLSQFEKWRPNQPDNFFATG 2015

Qy 116 SEVCVVMYHQPSAPAGIGGYPYMFQWNDRCNMKNFICKYS----DEKPAVPSREAECEE 171
Db 2016 EDCVVMWHERG-----EWNDVPCNYQLPFTCKKGTACGDDPPVVEHARTLGQK 2064

Qy 172 TE 173
Db 2065 KD 2066

RESULT 22
S57653
brevican precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
C;Accession: S57653
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning and sequence of mouse neurocan and brevican and their different e
A;Reference number: S57653
A;Accession: S57653
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-883 <RAU>
A;Cross-references: EMBL:X87096; NID:G886889; PIDN:CAA60575.1; PID:G886890
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EC
F;49-138/Domain: immunoglobulin homology <IMM>
F;173-250/Domain: link protein repeat homology <LNK1>
F;271-352/Domain: link protein repeat homology <LNK2>
F;626-657/Domain: EGF homology <EGF>
F;664-784/Domain: C-type lectin homology <LCH>
F;791-847/Domain: complement factor H repeat homology <FHD>

Query Match 13.3%; Score 147; DB 2; Length 883;
Best Local Similarity 29.7%; Pred. No. 6.2e-05;
Matches 43; Conservative 21; Mismatches 45; Indels 36; Gaps 8;

Qy 15 QRPCYKVIYFHDTSRRLLNFEEAKEACRRDGGQLVSISEDEQKLI-EKFIENLLPSDGDGF 73
Db 672 QGACYK---HFSTRR-SWEAEASQCRALGAHLTSICTPEEQDFVNDRYREYQ----- 719
Qy 74 WTCLRRREKQSNSTACQDLVAWTDGSGISQFRNYYVDEPS---CGSEVCVVM-YHQPSAP 129

Db 720 WIGL-----NDRTIEGDFLWSDGAPLLYENWNFGQPDYSYFLSGENCVVMVWHDQG-- 769
Qy 130 AGIGGYPYMFQWNDRCNMKNFICK 154
Db 770 -----QMSDVPVCNYHLSYTC 785

RESULT 23
LNRC1
lectin BRA3-1 precursor - barnacle (Megabalanus rosa)
C;Species: Megabalanus rosa
C;Date: 24-Feb-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: JCI503; A26094
R;Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, T.
Gene 128, 251-255, 1993
A;Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure and
A;Reference number: JCI503; MUID:93292994; PMID:8514190
A;Accession: JCI503
A;Molecule type: DNA; mRNA
A;Residues: 1-162 <TAK>
A;Cross-references: DDBJ:D13299
R;Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 874, 285-295, 1986
A;Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
A;Reference number: A26094
A;Accession: A26094
A;Molecule type: protein
A;Residues: 25-145, 'K', 147-162 <MUR>
A;Note: 146-Arg was also found
C;Comment: This galactose-binding lectin is isolated from the coelomic fluid.
C;Comment: This protein plays important roles in defense mechanisms and in development ar
C;Comment: The molecule is a tetramer of identical chains.
C;Genetics:
A;Introns: 22/1; 47/2; 86/3
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemolymph; homotetramer; lectin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-162/Product: lectin BRA3-1 #status experimental <MAT>
F;26-150/Domain: C-type lectin homology <LCH>
F;26-39, 56-150, 125-142/Disulfide bonds: #status experimental
F;157/Disulfide bonds: interchain (to 160) #status experimental
F;160/Disulfide bonds: interchain (to 157) #status experimental

Query Match 13.2%; Score 146.5; DB 1; Length 162;
Best Local Similarity 25.0%; Pred. No. 9.6e-06;
Matches 40; Conservative 26; Mismatches 59; Indels 35; Gaps 6;

Qy 3 LLSQPVCRGGTQPCVKVIYFHDTSRRLLNFEEAKEACR--RDGGQLVSISEDEQKLI 60
Db 19 ITTGECTCPGNLDWQYDGHYQVWSTYQVRWDAQLACQTVHPGAYLATIQSLENAFIS 78

Qy 61 KFIENLLPSDGDGF-WIGLRRREKQSNSTACQDLVAWTDGSGISQFRNYYVDEPS-----C 114
Db 79 ETVSN-----NRLWIGL-----NDIDLEGHYVWSNGEATDFTYWSNNPNNWENQDC 125

Qy 115 GSEVCVVMYHQPSAPAGIGGYPYMFQWNDRCNMKNFICK 154
Db 126 G-----VVNYDTVTG-----QWDDDDCCNKNRNFICK 151

RESULT 24
I50421
aggrecan precursor - chicken
N;Alternate names: cartilage chondroitin sulfate proteoglycan core protein
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072
R;Li, H.; Schwartz, N.B.; Vertel, B.M.
J. Biol. Chem. 268, 23504-23511, 1993
A;Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and
A;Reference number: A48884; MUID:94043149; PMID:8226878
A;Accession: I50421
A;Status: preliminary; translated from GB/EMBL/DDBJ

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:46:49 ; Search time 15.0369 Seconds
(without alignments)
706.418 Million cell updates/sec

Title: US-09-887-855-2_COPY_24_227
Perfect score: 1106
Sequence: 1 GRLLSGQPVCRGGTQRPCYK.....BEDAKKTFKESREALNLAY 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574	51.9	273	1	CHOD_MOUSE
2	561.5	50.8	273	1	CHOD_HUMAN
3	182	16.5	1456	1	MANR_HUMAN
4	177	16.0	1268	1	PGCN_MOUSE
5	176	15.9	1321	1	PGCN_HUMAN
6	174.5	15.8	3381	1	PGCV_BOVIN
7	174	15.7	1257	1	PGCV_RAT
8	174	15.7	2738	1	PGCV_RAT
9	174	15.7	3358	1	PGCV_MOUSE
10	174	15.7	3396	1	PGCV_HUMAN
11	171	15.5	3562	1	PGCV_CHICK
12	165	14.9	643	1	CD93_RAT
13	158.5	14.3	2364	1	PGCA_BOVIN
14	158.5	14.3	2415	1	PGCA_HUMAN
15	155.5	14.1	2333	1	PGCA_CANFA
16	154.5	14.0	612	1	LEM2_MOUSE
17	153.5	13.9	644	1	CD93_MOUSE
18	153.5	13.9	2124	1	PGCA_RAT
19	152	13.7	912	1	PGCB_BOVIN
20	151.5	13.7	652	1	CD93_HUMAN
21	151	13.7	197	1	CLE1_HUMAN
22	149	13.5	321	1	FCE2_HUMAN
23	147.5	13.3	2132	1	PGCA_MOUSE
24	147	13.3	883	1	PGCB_MOUSE
25	146	13.2	2109	1	PGCA_CHICK
26	145	13.1	158	1	LECG_TRIST
27	145	13.1	883	1	PGCB_RAT
28	144.5	13.1	173	1	LEC2_MEGRO
29	144.5	13.1	372	1	LEM1_RAT
30	143.5	13.0	372	1	LEM1_MOUSE
31	141.5	12.8	331	1	FCE2_MOUSE
32	141.5	12.8	549	1	LEM2_RAT
33	140.5	12.7	162	1	LEC3_MEGRO
34	140	12.7	370	1	LEM1_BOVIN
35	139	12.6	248	1	PSPA_HUMAN
36	139	12.6	283	1	LECA_SARPE
37	138.5	12.5	152	1	IXA_TRIFL
38	138.5	12.5	202	1	TETN_MOUSE
39	137.5	12.4	372	1	LEM1_MACMU
40	137.5	12.4	372	1	LEM1_PAPHA
41	136	12.3	175	1	LITH_BOVIN
42	135	12.2	165	1	LIT1_MOUSE
43	134.5	12.2	132	1	ACAL_ANSAN
44	134.5	12.2	372	1	LEM1_PONPY
45	134.5	12.2	485	1	LEM2_BOVIN

ALIGNMENTS

RESULT 1
CHOD_MOUSE STANDARD; PRT; 273 AA.
AC Q9CXM0; Q8VI31;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chondrolectin precursor (Transmembrane protein MT75).
GN CHODL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Weng L., Smits P., Hubner R., Wouters J., Merregaert J.;
RT "Mt75, a low expressed c-type lectin gene involving in
RT chondrogenesis".
RL Submitted (OCT-2000) to the EMBL/GenBank/DBBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glissi C., King S., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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EMBL; AF311699; AAL50354.1; -.

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DR EMBL; AK014255; BAB29226.1; -.
DR HSSP; P22897; 1EGG.
DR MGI; 2179069; Chodl.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 273 CHONDROLECTIN.
FT DOMAIN 22 216 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 217 237 POTENTIAL.
FT DOMAIN 238 273 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 35 179 C-TYPE LECTIN.
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 24 24 V -> W (IN REF. 2).
FT CONFLICT 179 179 T -> K (IN REF. 2).
SQ SEQUENCE 273 AA; 30303 MW; E052D933F244F4C7 CRC64;

Query Match 51.9%; Score 574; DB 1; Length 273;
Best Local Similarity 57.4%; Pred. No. 2.3e-44;
Matches 109; Conservative 26; Mismatches 41; Indels 14; Gaps 5;

Qy 2 RLISGQPCVRCGGTQPCVKVIYFHTSRRLNFEBAKEACRRDGGQLVSISEDEQKLIK 61
Db 23 RVVSGQKVCFAVDKPCYKAYFHELSRVSFQEARLACESEGGVLLSLENAEQKLIES 82

Qy 62 FIENLLP-----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSIQPRNWWVDEPSCGS 116
Db 83 MLQNLTKPGTGISDGDGFWIGLRRSGDGT-SGACPDLYQWSDGSSQPRNWWTDEPSCGS 141

Qy 117 EVCVVMYHQPSAPAGIGGPMFQWQNDRCNMKNFICKYSDE-KPAVPSREAEGETELT 175
Db 142 EKCVVMYHQPTANPLGLGPPYLYQWNDRCNMKNHYICTYPEIHPTEPA-----EKPYL 196

Qy 176 TPVLPEETQE 185
Db 197 NQ--PEETHE 204

RESULT 2
CHOD_HUMAN STANDARD; PRT; 273 AA.
AC Q9H9P2; Q9HCY3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Chondrolectin precursor (Transmembrane protein MT75) (Protein PRED12).
GN CHODL OR C21ORF68.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=22074930; PubMed=12079284;
RA Weng L., Smits P., Wauters J., Merregaert J.;
RT "Molecular cloning and characterization of human chondrolectin, a
RL novel type I transmembrane protein homologous to C-type lectins.";
RL Genomics 80:62-70(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyma S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordtsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
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RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 27-273 FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Takiguchi S.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP TISSUE SPECIFICITY.
RX MEDLINE=21564202; PubMed=11707072;
RA Raymond A., Friedli M., Neergard Henriksen C., Chapot F., Deutsch S.,
RA Ucla C., Rossier C., Lyle R., Guipponi M., Antonarakis S.E.;
RT "From PREDS and open reading frames to cDNA isolation: revisiting the
RT human chromosome 21 transcription map.";
RL Genomics 78:46-54(2001).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Found in spleen, testis, prostate and fetal
CC liver. Expression limited to vascular muscle of testis, smooth
CC muscle of prostate stroma, heart muscle, skeletal muscle, crypts
CC of small intestine, and red pulp of spleen.
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
CC EMBL; AF257472; AAL05981.1; -.
CC EMBL; AL163217; CAB90388.1; -.
CC EMBL; BC009418; AAH09418.1; -.
CC EMBL; AK022689; BAB14181.1; ALT_INIT.
CC HSSP; P22897; 1EGG.
CC Genew; HGNC:17807; CHODL.
CC MIM; 607247; -.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin_c; 1.
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DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 6.
DR PROSITE; PS00441; C-TYPE LECTIN 2; 8.
DR PROSITE; PS00023; FIBRONECTIN 2; 1.
DR PROSITE; PS00231; RICIN B LECTIN; 1.
KW Receptor; Signal; Calcium-binding; Transmembrane; Repeat;
KW Glycoprotein; Endocytosis; Macrophage; Lectin; Antigen; 3D-structure.
FT SIGNAL 1
FT CHAIN 18
FT DOMAIN 19 1456 MACROPHAGE MANNOS RECEPTOR.
FT DOMAIN 19 1383 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1384 1411 POTENTIAL.
FT DOMAIN 1412 1456 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 142 RICIN B-TYPE LECTIN.
FT DOMAIN 157 212 FIBRONECTIN TYPE-II.
FT DOMAIN 216 344 C-TYPE LECTIN 1 (LONG FORM).
FT DOMAIN 360 490 C-TYPE LECTIN 2 (LONG FORM).
FT DOMAIN 502 629 C-TYPE LECTIN 3 (LONG FORM).
FT DOMAIN 644 781 C-TYPE LECTIN 4 (LONG FORM).
FT DOMAIN 805 926 C-TYPE LECTIN 5 (LONG FORM).
FT DOMAIN 943 1083 C-TYPE LECTIN 6 (LONG FORM).
FT DOMAIN 1100 1216 C-TYPE LECTIN 7 (LONG FORM).
FT DOMAIN 1228 1359 C-TYPE LECTIN 8 (LONG FORM).
FT DISULFID 646 659
FT DISULFID 680 777
FT DISULFID 753 769
FT CARBOHYD 104 104
FT CARBOHYD 344 344
FT CARBOHYD 529 529
FT CARBOHYD 926 926
FT CARBOHYD 930 930
FT CARBOHYD 1160 1160
FT CARBOHYD 1205 1205
FT CARBOHYD 1311 1311
FT TURN 648 649
FT STRAND 651 652
FT TURN 654 655
FT STRAND 658 663
FT HELIX 667 669
FT STRAND 671 671
FT HELIX 673 683
FT TURN 684 684
FT STRAND 686 687
FT HELIX 693 705
FT TURN 706 707
FT TURN 709 710
FT STRAND 712 718
FT TURN 723 724
FT STRAND 727 727
FT TURN 729 730
FT STRAND 733 733
FT TURN 741 742
FT HELIX 746 748
FT STRAND 752 757
FT TURN 758 761
FT STRAND 764 768
FT TURN 769 770
FT STRAND 773 780
FT TURN 781 782
SQ SEQUENCE 1456 AA; 166011 MW; 264E5AF3C576A5E3 CRC64;

Query Match
Best Local Similarity 16.5%; Score 182; DB 1; Length 1456;
Matches 52; Conservative 37; Mismatches 61; Indels 54; Gaps 8;

QY 19 YKVIYFHDTSRLNFEAEKACRDRGQGLVSIQSEDEQKLEKFIENLLPSDGFWIGLR 78
DB 807 YKDYQYFSEKKEKTMNDNARAFCKRNFGLVSIQSESEKFLWKYV-NRNDASAYFIGLL 865
QY 79 RREEKQSNSTACQDLAYWTDGSIQPRNWWYVDEPSGCS--EVCVWYHQPSAPAGIGGPY 136
DB 866 ISLDKK-----FAWMDGSKVDYVSWATGEPNFANEDENCVTMY-----SNSGF---- 908

QY 137 MFQWDDRCNMKNPICKYSDEK-----PAVPSREAGEETEELTTPVLPEETQE----- 185
DB 909 ---WNDINGYPNAPICQHNSSINATTMP-----TMPSPVSGCKEGWNFYSN 954
QY 186 -----EDAKTKFKESREAAAL 200
DB 955 KCFKIFGFMEERKNWQEARACI 978

RESULT 4
PGCN_MOUSE
ID PGCN_MOUSE STANDARD; PRT; 1268 AA.
AC P55066;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
GN CSPG3 OR NCAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=96039250; PubMed=7490074;
RA Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.,
RA Faessler R.;
RT "Structure and chromosomal localization of the mouse neurocan gene.";
RL Genomics 28:405-410(1995).
CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
CC development by binding to neural cell adhesion molecules (NG-CAM
CC and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
CC acid.
CC -!- TISSUE SPECIFICITY: Brain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC
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CC
CC -----
CC EMBL; X84727; CAA59216.1; -
CC PIR; S52781; S52781.
CC HSSP; P00740; 1EDM.
CC MGD; MGI:104694; Cspg3.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR00152; Asx_hydroxyl_s.
CC InterPro; IPR000742; EGF 2.
CC InterPro; IPR01881; EGF_Ca.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR01304; Lectin_C.
CC InterPro; IPR00538; Link.
CC InterPro; IPR00436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 2.
CC PRINTS; PR00356; ANTIFREEZEII.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 2.
CC SMART; SM00032; CCP; 1.

DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
FT EGF-like domain; Calcium; Repeat; Lentin; Sushi; Signal; Polymorphism.
FT SIGNAL 1 22
FT CHAIN 23 1321
FT DOMAIN 38 153
FT DOMAIN 159 254
FT DOMAIN 260 356
FT DOMAIN 1008 1044
FT DOMAIN 1046 1082
FT DOMAIN 1084 1213
FT DOMAIN 1214 1272
FT DISULFID 59 140
FT DISULFID 182 253
FT DISULFID 206 227
FT DISULFID 280 355
FT DISULFID 304 325
FT DISULFID 1012 1023
FT DISULFID 1017 1032
FT DISULFID 1034 1043
FT DISULFID 1088 1099
FT DISULFID 1116 1208
FT DISULFID 1184 1200
FT DISULFID 1215 1258
FT DISULFID 1244 1271
FT CARBOHYD 122 122
FT CARBOHYD 340 340
FT CARBOHYD 1026 1026
FT CARBOHYD 1223 1223
FT VARIANT 1254 1254
FT CONFLICT 1234 1234
FT CONFLICT 1282 1282
FT SEQUENCE 1321 AA; 142972 MW; 2EF47F823DB980B8 CRC64;
SQ
Query Match 15.9%; Score 176; DB 1; Length 1321;
Best Local Similarity 31.5%; Pred. No. 9.6e-08;
Matches 45; Conservative 18; Mismatches 48; Indels 32; Gaps 6;
QY 15 QPCYKVIYFHTSRRLNFEAEACRRDGGQGVSTSESEDEQLIEKFIENLLPSDGF 74
Db 1096 QGHCYR--YF---ARRAWEDAEDKDCRRSGHLTSVHSPEEHSFINSF-----GHENTW 1144
QY 75 IGLRRREKQSNSTACQILYAWTDGSIQFRNWWYDEPS---CGSEVCVMVYHQSAPAG 131
Db 1145 IGLNDRIVERD-----FQWTDNTGLQFENWRENQPDNFFAGGEDCVMVVAHESG--- 1193
QY 132 IGGPYMFQWDDRCNMKNPFICK 154
Db 1194 -----RWNDVPCNVLFPVCK 1209
RESULT 6
PGCV BOVIN
ID PGCV BOVIN STANDARD; PRT; 3381 AA.
AC P81282; O77609; O77610; O77611; O77612;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Versican core protein precursor (large fibroblast proteoglycan)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
DE hyaluronate-binding protein) (GHAP).
GN CPBG2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS VO; V1; V2 AND V3).
RC TISSUE=Forebrain;

RX MEDLINE=98288320; PubMed=9624174;
RA Schmalfeldt M., Dours-Zimmermann M.T., Winterhalter K.H.,
RA Zimmermann D.R.;
RT "Versican V2 is a major extracellular matrix component of the mature
RT bovine brain.";
RL J. Biol. Chem. 273:15758-15764 (1998).
RN [2]
RP SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
RP AND 342-348.
RC TISSUE=Spinal cord;
RX MEDLINE=92062692; PubMed=1720020;
RA Perides G., Biviano F., Bignami A.;
RT "Interaction of a brain extracellular matrix protein with hyaluronic
RT acid.";
RL Biochim. Biophys. Acta 1075:248-258 (1991).
CC -!- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -!- SUBUNIT: Interacts with FBLN1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=P81282-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=P81282-2; Sequence=VSP_003078, VSP_003079;
CC Name=V2;
CC IsoId=P81282-3; Sequence=VSP_003080;
CC Name=V3;
CC IsoId=P81282-4; Sequence=VSP_003078, VSP_003081;
CC -!- TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 are expressed
CC in the central nervous system, and in a number of mesenchymal and
CC epithelial tissues; the major isoform V2 is restricted to the
CC central nervous system.
CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
CC (By similarity).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF060456; AAC24358.1; -.
CC EMBL; AF060457; AAC24359.1; -.
CC EMBL; AF060458; AAC24360.1; -.
CC EMBL; AF060459; AAC24361.1; -.
CC PIR; T14274; T14274.
CC PIR; T42389; T42389.
CC HSSP; P01132; 1EPG.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR001304; Lentin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00047; ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF00084; sushi; 1.

DR PFam; PF00193; Xlink; 2.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 3381
FT DOMAIN 21 147
FT DOMAIN 168 245
FT DOMAIN 266 347
FT DOMAIN 349 1336
FT DOMAIN 1337 3074
FT DOMAIN 3074 3110
FT DOMAIN 3112 3148
FT DOMAIN 3161 3275
FT DOMAIN 3280 3338
FT DISULFID 44 131
FT DISULFID 173 244
FT DISULFID 197 218
FT DISULFID 271 346
FT DISULFID 295 316
FT DISULFID 3078 3089
FT DISULFID 3083 3098
FT DISULFID 3100 3109
FT DISULFID 3116 3127
FT DISULFID 3121 3136
FT DISULFID 3138 3147
FT DISULFID 3154 3165
FT DISULFID 3182 3274
FT DISULFID 3250 3266
FT DISULFID 3281 3324
FT DISULFID 3310 3337
FT CARBOHYD 57 57
FT CARBOHYD 331 331
FT CARBOHYD 352 352
FT CARBOHYD 817 817
FT CARBOHYD 965 965
FT CARBOHYD 1017 1017
FT CARBOHYD 1333 1333
FT CARBOHYD 1393 1393
FT CARBOHYD 1437 1437
FT CARBOHYD 1463 1463
FT CARBOHYD 1653 1653
FT CARBOHYD 1974 1974
FT CARBOHYD 2045 2045
FT CARBOHYD 2074 2074
FT CARBOHYD 2103 2103
FT CARBOHYD 2263 2263
FT CARBOHYD 2290 2290
FT CARBOHYD 2356 2356
FT CARBOHYD 2623 2623
FT CARBOHYD 2641 2641
FT CARBOHYD 2919 2919
FT CARBOHYD 3052 3052
FT CARBOHYD 3354 3354
FT CARBOHYD 3364 3364
FT VARSPLIC 349 349
P -> R (in isoform V1 and isoform V3).

FT VARSPLIC 350 1336 /FTid=VSP 003078.
FT Missing (in isoform V1).
FT /FTid=VSP 003079.
FT VARSPLIC 1337 3074 Missing (in isoform V2).
FT /FTid=VSP 003080.
FT VARSPLIC 350 3074 Missing (in isoform V3).
FT /FTid=VSP 003081.
FT CONFLICT 25 25 MISSING (IN REF. 2).
FT CONFLICT 51 51 MISSING (IN REF. 2).
FT CONFLICT 89 89 N -> D (IN REF. 2).
FT CONFLICT 96 96 Q -> D (IN REF. 2).
FT CONFLICT 346 346 C -> R (IN REF. 2).
SQ SEQUENCE 3381 AA; 369984 MW; F09716FA7778D459 CRC64;
Query Match 15.8%; Score 174.5; DB 1; Length 3381;
Best Local Similarity 25.5%; Pred. No. 4.2e-07;
Matches 59; Conservative 26; Mismatches 71; Indels 75; Gaps 11;
QY 15 QRPCYKVIYFHDTSRRLLNPFEEAKEACRRDGGQLVSIIESEDEQKLEKFIENLLPSDGF- 73
Db 3162 QGQCYK--YF---AHRRTWDAARECRLQGAHLTSILSHEEQMFVNRV-----GHDYQ 3209
QY 74 WIGLRRREKQSNSTACQDLYAWTDGSIQFRNWTYDEP-----SCGSEVCVVMYHQPSAP 129
Db 3210 WIGL-----NDKMFHDFRWTGDTLQYENWRPNQPDSPFFSTGDCVVIWHENG-- 3259
QY 130 AGIGGYPYMFQWDDRCNMKNFICKYS-----DEKPAVPSREAEGE----- 170
Db 3260 -----QWNDVPCNYHLTYTCKKGTACGQPPVVENAKTFGKMKPRYEINSLRYHC 3310
QY 171 -----ETELTT-----PVL-----PEETQEEDAKTFKESREAAALN 201
Db 3311 KDGFIQRHLPTIRCLNGRWAMPKITCLNPSAYQRTYSKKYFKNSSAKDN 3361
RESULT 7
PGCN_RAT STANDARD; PRT; 1257 AA.
AC P55067;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
DE (245 kDa early postnatal core glycoprotein) [Contains: 150 kDa adult
core glycoprotein].
GN CSPG3 OR NCAN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=92406907; PubMed=1326557;
RA Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
RT "Cloning and primary structure of neurocan, a developmentally
regulated, aggregating chondroitin sulfate proteoglycan of brain.";
RL J. Biol. Chem. 267:19536-19547(1992).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=94230574; PubMed=7513709;
RA Friedlander D.R., Milev P., Karthikeyan L., Margolis R.K.,
RA Margolis R.U., Grumet M.;
RT "The neuronal chondroitin sulfate proteoglycan neurocan binds to the
neuronal cell adhesion molecules Ng-CAM/L1/NILE and N-CAM, and inhibits
neuronal adhesion and neurite outgrowth.";
RL J. Cell Biol. 125:669-680(1994).
CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
development by binding to neural cell adhesion molecules (NG-CAM
and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
acid.
CC -!- TISSUE SPECIFICITY: Early postnatal and adult brain; not expressed
in kidney, lung, liver and muscle.

-!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
-!- PTM: TWO ISOFORMS WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC DEGRADATION. THE LARGE ISOFORM IS PREDOMINANT IN EARLY POSTNATAL BRAIN, THE SMALL ISOFORM IS FOUND IN ADULT BRAIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

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EMBL; M97161; AAC37679.1; --
PIR; S28764; S28764.
HSSP; P00740; LEDM.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR000152; Asx hydroxyl_s.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR007110; Ig_Like.
InterPro; IPR003599; Ig.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 2.
Pfam; PF00047; Ig; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
PRINTS; PRO0356; ANTIFREEZEII.
PRINTS; PRO1265; LINKMODULE.
ProDom; PD000918; Link; 2.
SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00409; IG_1.
SMART; SM00445; LINK; 2.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
PROSITE; PS00022; EGF_1; 3.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
SIGNAL 1 22
CHAIN 23 1257 NEUROCAN CORE PROTEIN.
CHAIN 639 1257 150 kDa ADULT CORE GLYCOPROTEIN.
DOMAIN 37 157 IG-LIKE V-TYPE.
DOMAIN 158 253 LINK 1.
DOMAIN 259 355 LINK 2.
DOMAIN 949 985 EGF-LIKE 1.
DOMAIN 987 1023 EGF-LIKE 2.
DOMAIN 1025 1154 C-TYPE LECTIN.
DOMAIN 1155 1213 SUSHI.
DOMAIN 58 139 BY SIMILARITY.
DISULFID 181 252 BY SIMILARITY.
DISULFID 205 226 BY SIMILARITY.
DISULFID 279 354 BY SIMILARITY.
DISULFID 303 324 BY SIMILARITY.
DISULFID 953 964 BY SIMILARITY.

FT DISULFID 958 973 BY SIMILARITY.
FT DISULFID 975 984 BY SIMILARITY.
FT DISULFID 1029 1040 BY SIMILARITY.
FT DISULFID 1057 1149 BY SIMILARITY.
FT DISULFID 1125 1141 BY SIMILARITY.
FT DISULFID 1156 1199 BY SIMILARITY.
FT DISULFID 1185 1212 BY SIMILARITY.
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 737 737 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 944 944 O-LINKED (XYL. . .) (CHONDROITIN SULFATE).
FT CARBOHYD 967 967 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1164 1164 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1257 AA; 135544 MW; 992B333DCFA19EE1B CRC64;

Query Match 15.7%; Score 174; DB 1; Length 1257;
Best Local Similarity 30.8%; Pred. No. 1.4e-07;
Matches 44; Conservative 18; Mismatches 49; Indels 32; Gaps 6;

QY 15 QRPCYKVIYFHTSRLNPFEEAKEACRRDGGQLVSISEDEQKLEKFIENLLPSDGEFW 74
Db 1037 QGHYR--YF---AHRRAWDAERDCRRRAGHLTSVHSPEHKFINSF-----GHENSW 1085

QY 75 IGLRRREEKQSNSTACQDLYAWTDGSIQSFRNRYVDEPS---CGSEVCVVMYHQPSAPAG 131
Db 1086 IGLNDRTVERD-----FQWTDNTGLQYENWREKQPDNFFAGGEDCVVMVAHENG--- 1134

QY 132 IGGPYMFQWNDRCNMKNFICK 154
Db 1135 -----RWNDVPCVNYNLPYVCK 1150

RESULT 8
PGCV_RAT
ID_PGCV_RAT STANDARD; PRT; 2738 AA.
AC Q9ERB4; O08592; O88564; Q9R1K4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Versican core protein precursor (Large fibroblast proteoglycan)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
DE hyaluronate-binding protein) (GHAP) (Fragments).
GN CP5G2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 349-2738 FROM N.A. (ISOFORM V0), SEQUENCE FROM N.A.
RP (ISOFORM V3), AND SEQUENCE OF 2657-2738 FROM N.A. (ISOFORM VINT).
RC STRAIN=Wistar Kyoto;
RX MEDLINE=99327053; PubMed=10397680;
RA Lemire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,
RA Wight T.N.;
RT "Versican/PG-M isoforms in vascular smooth muscle cells.";
RL Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
RN [2]
RP SEQUENCE OF 349-2738 FROM N.A. (ISOFORM V0).
RC STRAIN=Wistar Kyoto;
RX MEDLINE=98308094; PubMed=9642104;
RA Milev P., Maurel P., Chiba A., Mevissen M., Popp S., Yamaguchi Y.,
RA Margolis R.K., Margolis R.U.;
RT "Differential regulation of expression of hyaluronan-binding
RT proteoglycans in developing brain: aggrecan, versican, neurocan, and
RT brevican.";
RL Biochem. Biophys. Res. Commun. 247:207-212(1998).
RN [3]
RP SEQUENCE OF 2421-2463 FROM N.A. (ISOFORM V0).
RC TISSUE=Kidney;
RX MEDLINE=98094159; PubMed=9434070;
RA Pyke C., Kristensen P., Ostergaard P.B., Oturai P.S., Romer J.;
RT "Proteoglycan expression in the normal rat kidney.";
RL Nephron 77:461-470(1997).

[4]
SEQUENCE OF 2535-2738 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Lung;
Blomberg L.A., Chan W.-Y., Clerch L., Massaro D.;
"Molecular cloning and characterization of two developmentally
regulated genes in rat lung.";
Submitted (SBP-2000) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: May play a role in intercellular signaling and in
connecting cells with the extracellular matrix. May take part in
the regulation of cell motility, growth and differentiation. Binds
hyaluronic acid.
-!- SUBUNIT: Interacts with FBLN1 (By similarity).
-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist;
Name=V0;
IsoId=Q9ERB4-1; Sequence=Displayed;
Name=V3;
IsoId=Q9ERB4-2; Sequence=VSP_003091;
Name=Vint;
IsoId=Q9ERB4-3; Sequence=VSP_003092;
-!- TISSUE SPECIFICITY: In kidney is expressed in the papillary area,
but not in glomeruli.
-!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
(By similarity).
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 link domains.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

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EMBL; AF062402; AAC40166.1; -.
EMBL; U75306; AAB51125.1; -.
EMBL; AF084544; AAD48544.1; -.
EMBL; AF072892; AAC26116.1; -.
EMBL; AY007691; AAG16631.1; -.
HSSP; P01132; 1EPG.
InterPro; IPR000152; Asx hydroxyl_s.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR007110; IG-like.
InterPro; IPR003599; IG.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
PRINTS; PR01265; LINKMODULE.
ProDom; PD000918; Link; 2.
SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 2.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;

KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 2738 VERSICAN CORE PROTEIN.
FT NON_CONS 348 349
FT DOMAIN 21 146 IG-LIKE V-TYPE.
FT DOMAIN 167 244 LINK 1.
FT DOMAIN 265 346 LINK 2.
FT DOMAIN <349 695 GAG-ALPHA
(GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN).
FT DOMAIN 696 2431 GAG-BETA.
FT DOMAIN 2431 2467 EGF-LIKE 1.
FT DOMAIN 2469 2505 EGF-LIKE 2, CALCIUM-BINDING.
FT DOMAIN 2518 2632 C-TYPE LECTIN.
FT DOMAIN 2637 2695 SUSHI.
FT DISULFID 44 130 BY SIMILARITY.
FT DISULFID 172 243 BY SIMILARITY.
FT DISULFID 196 217 BY SIMILARITY.
FT DISULFID 270 345 BY SIMILARITY.
FT DISULFID 294 315 BY SIMILARITY.
FT DISULFID 2435 2446 BY SIMILARITY.
FT DISULFID 2440 2455 BY SIMILARITY.
FT DISULFID 2457 2466 BY SIMILARITY.
FT DISULFID 2473 2484 BY SIMILARITY.
FT DISULFID 2478 2493 BY SIMILARITY.
FT DISULFID 2495 2504 BY SIMILARITY.
FT DISULFID 2511 2522 BY SIMILARITY.
FT DISULFID 2539 2631 BY SIMILARITY.
FT DISULFID 2607 2623 BY SIMILARITY.
FT DISULFID 2638 2681 BY SIMILARITY.
FT DISULFID 2667 2694 BY SIMILARITY.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 692 692 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 758 758 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 802 802 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 805 805 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1257 1257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1435 1435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1633 1633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1660 1660 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1684 1684 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1738 1738 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1848 1848 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2004 2004 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2409 2409 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2711 2711 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2721 2721 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 349 2431 Missing (in isoform V3).
FT VARSPLIC 2697 2738 /FTId=VSP_003091.
FT VARSPLIC 2738 PSAYQRTYVKYKLYKNSSSVKDNSINTSKHEHRSRRWQETR
R -> RKWSFRKNGQPCFNKY (in isoform Vint).
FT CONFLICT 2535 2539 AEREC -> NSARG (IN REF. 4).
FT SEQUENCE 2738 AA; 300004 MW; 12CA626D58BD8C6A CRC64;
/FTId=VSP_003092.
SQ
Query Match 15.7%; Score 174; DB 1; Length 2738;
Best Local Similarity 28.5%; Pred. No. 3.6e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
QY 15 QRPCYKVIYFHTSRRRLNFEFEAKACRRDGGQLVSISEDEQKLIKFIENLLPSDGF- 73
Db 2519 QGQCYK--YF---AHRRTWDAARECRLOGAHLTSILSHEEQMFVNRV-----GHDYQ 2566
QY 74 WGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEP----SCGSEVCVMYHQPSAP 129
Db 2567 WIGL-----NDKMFHDHFRWTDGSAIQYENWRPNQDPSFFSAGDCVVIWHENG-- 2616
QY 130 AGIGGPMFMQWDDRCNMKNFICKYS-----DEKPAVPSREAEGE 170
Db 2617 -----QWNVPCNYHLTYTCKKGIACGQPPVVENAKTFGK 2652

RESULT 11

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PGCV_CHICK
ID_PGCV_CHICK STANDARD; PRT; 3562 AA.
AC Q90953; Q90945;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Versican core protein precursor (large fibroblast proteoglycan)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
GN CPSG2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS V0 AND V1).
RC STRAIN=White leghorn; TISSUE=Limb bud;
RX MEDLINE=93300846; PubMed=8314802;
RA Shinomura T., Nishida Y., Ito K., Kimata K.;
RT "cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan
RT expressed during chondrogenesis in chick limb buds. Alternative
RT spliced multiforms of PG-M and their relationships to versican.";
RL J. Biol. Chem. 268:14461-14469(1993).
CC -!- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=Q90953-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=Q90953-2; Sequence=VSP_003093;
CC -!- TISSUE SPECIFICITY: Prechondrogenic condensation area of
CC developing limb buds.
CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
CC (By similarity).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -----
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CC -----
DR EMBL; X60226; CAA42787.1; -.
DR EMBL; D13542; BAA02742.1; -.
DR PIR; A47171; A47171.
DR HSSP; P00740; 1EDM.
DR InterPro; IPR000152; Asx_hydroxyl_s.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 1.
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DR Pfam; PF00193; Xlink; 2.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 3562 VERSICAN CORE PROTEIN.
FT DOMAIN 27 143 IG-LIKE V-TYPE.
FT DOMAIN 166 243 LINK 1.
FT DOMAIN 264 345 LINK 2.
FT DOMAIN 3254 3290 EGF-LIKE 1.
FT DOMAIN 3292 3328 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3341 3455 C-TYPE LECTIN.
FT DOMAIN 3460 3518 SUSHI.
FT DISULFID 44 129 BY SIMILARITY.
FT DISULFID 171 242 BY SIMILARITY.
FT DISULFID 195 216 BY SIMILARITY.
FT DISULFID 269 344 BY SIMILARITY.
FT DISULFID 293 314 BY SIMILARITY.
FT DISULFID 3258 3269 BY SIMILARITY.
FT DISULFID 3263 3278 BY SIMILARITY.
FT DISULFID 3280 3289 BY SIMILARITY.
FT DISULFID 3296 3307 BY SIMILARITY.
FT DISULFID 3301 3316 BY SIMILARITY.
FT DISULFID 3318 3327 BY SIMILARITY.
FT DISULFID 3334 3345 BY SIMILARITY.
FT DISULFID 3362 3454 BY SIMILARITY.
FT DISULFID 3430 3446 BY SIMILARITY.
FT DISULFID 3461 3504 BY SIMILARITY.
FT DISULFID 3490 3517 BY SIMILARITY.
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 709 709 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 948 948 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1409 1409 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1479 1479 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1530 1530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1625 1625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1751 1751 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1988 1988 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2088 2088 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2089 2089 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2507 2507 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2642 2642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2679 2679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2748 2748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2762 2762 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3069 3069 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3194 3194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3232 3232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 3545 3545 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 485 1411 Missing (in isoform V1).
FT SEQUENCE 3562 AA; 388078 MW; 9BC566E88C1602D2 CRC64;
FT /FTIG=VSP_003093.
```

Query Match 15.5%; Score 171; DB 1; Length 3562;
Best Local Similarity 28.5%; Pred. No. 9.2e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;

QY 15 QRCYKVIYFHTDTRRLNFEAEACRRDGGQLVSIIESEDEQKLEKFIENLLPSDGF- 73
Db 3342 QGQYK--YF---AHRRTWDTARECRLOGAHLTSILSHEEQVFNRI-----GHDIQ 3389

QY 74 WIGLRREKQSNSTACQDLYAWTDGSIQFRNMYVDEP-----SCGSEVCVVMYHQPAP 129
Db 3390 WIGL-----NDKMFERDFRWTGSLQYENWRPNQDPSFFSAGEDCVVLIWHENG-- 3439

QY 130 AGIGGPMYFQWDDRCNMKNFICKYS-----DEKPAVPSREAGE 170
Db 3440 -----QWNDVPCNYHLTYCKGTACGQPPVVENAKTFGR 3475

RESULT 12

CD93_RAT STANDARD; PRT; 643 AA.
ID CD93_RAT
AC Q9ET6L; Q9J126;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Complement component C1q receptor precursor (Complement component 1, q
DE subcomponent, receptor 1) (C1qR) (C1qR(p)) (C1q/MBL/SPA receptor)
DE (CD93 antigen) (Cell surface antigen AA4).
GN C1QR1 OR CD93 OR C1QRP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PVG; TISSUE=Natural killer cells;
RX MEDLINE=20545218; PubMed=11093152;
RA Lovik G., Vaage J.T., Dissen E., Szpirer C., Ryan J.C., Rolstad B.;
RT "Characterization and molecular cloning of rat C1qR, a receptor on NK
RT cells.";
RL Eur. J. Immunol. 30:3355-3362(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Lung;
RX MEDLINE=20507883; PubMed=10934210;
RA Dean Y.D., McGreal E.P., Akatsu H., Gasque P.;
RT "Molecular and cellular properties of the rat AA4 antigen, a C-type
RT lectin-like receptor with structural homology to thrombomodulin.";
RL J. Biol. Chem. 275:34382-34392(2000).
CC -!- FUNCTION: Receptor (or element of a larger receptor complex) for
CC C1q, mannose-binding lectin (MBL2) and pulmonary surfactant
CC protein A (SPA). May mediate the enhancement of phagocytosis in
CC monocytes and macrophages upon interaction with soluble defense
CC collagens. May play a role in intercellular adhesion.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed. Highly expressed in lung and
CC heart. Expressed at lower level in brain, thymus, liver, spleen,
CC intestine, kidney, adrenal gland, muscle and testis. Expressed on
CC endothelial cells, platelets, undifferentiated monocytes and
CC circulating natural killer cells.
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 5 EGF-like domains.
CC
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CC
CC EMBL; AF136537; AAG01572.1; -;
CC EMBL; AF160978; AAF80402.1; -;

DR HSSP; P35555; 1EMN
DR GO; GO:0016021; C: integral to membrane; ISS.
DR GO; GO:0004872; F: receptor activity; ISS.
DR GO; GO:0016337; P: cell-cell adhesion; ISS.
DR GO; GO:0042116; P: macrophage activation; ISS.
DR GO; GO:0006909; P: phagocytosis; ISS.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 3.
KW Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
KW EGF-like domain; Lectin; Glycoprotein.
FT SIGNAL 1 23
FT CHAIN 24 643
FT DOMAIN 24 571
FT TRANSMEM 572 592
FT DOMAIN 593 643
FT DOMAIN 31 173
FT DOMAIN 257 298
FT DOMAIN 299 341
FT DOMAIN 342 381
FT DOMAIN 382 423
FT DOMAIN 424 462
FT DISULFID 261 272
FT DISULFID 268 282
FT DISULFID 284 297
FT DISULFID 303 314
FT DISULFID 308 325
FT DISULFID 327 340
FT DISULFID 346 355
FT DISULFID 351 364
FT DISULFID 366 380
FT DISULFID 386 397
FT DISULFID 393 406
FT DISULFID 408 422
FT DISULFID 428 437
FT DISULFID 433 446
FT DISULFID 448 461
FT CARBOHYD 322 322
FT CARBOHYD 498 498
FT CONFLICT 417 417
SQ SEQUENCE 643 AA; 68781 MW; 9AE4C933AD943DB6 CRC64;

Query Match 14.9%; Score 165; DB 1; Length 643;
Best Local Similarity 25.2%; Pred. No. 3.8e-07;
Matches 52; Conservative 35; Mismatches 73; Indels 46; Gaps 10;

QY 1 GRLLSGQP-----VCRGGTQRCYKVIYFHTDTRRLNFEAEACRRDGGQLVSIIESED 54
Db 15 GQLWAGAAADSEAVVCEG---TACYTAHW-----GKLSAAEAQHRCNENGGLATVKSEE 66

QY 55 EQKLEKFIENLL-----PSD---GDFWIGLRREKQSNSTACQDLYAWT-DGSIQFRN 106
Db 67 EARHVQEALAQLLKTKAPSETKIGKFWIGLQREKGTCTYHDLPMKGFWSWGGEDDTYSN 126

QY 107 WY-VDEPSCGSEVCVVMY-----HQPSAPAGIGGPMYFQWDDRC-----NMKNF 151
Db 127 WYKASKSSCISKRCVSLILDLSLKPSPHLP-----KWHPGCTPDAPGNSIEGF 177

QY 152 ICKYSDEKPAVPSREAGEETEITTP 177
Db 178 LCKFNFKGMCSPALGPGQQLTYTTP 203

```
RESULT 13
PGCA_BOVIN
ID PGCA_BOVIN STANDARD; PRT; 2364 AA.
AC P13608; P79117; Q28159;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
DE protein) (CSPCP).
GN AGC1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hering T.M., Kollar J., Huynh T.D.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=89380219; PubMed=2528543;
RA Antonsson P., Heinegaard D., Oldberg A.;
RT "The keratan sulfate-enriched region of bovine cartilage proteoglycan
RT consists of a consecutively repeated hexapeptide motif.";
RL J. Biol. Chem. 264:16170-16173(1989).
RN [3]
RP SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
RX MEDLINE=87270630; PubMed=3111460;
RA Oldberg A., Antonsson P., Heinegaard D.;
RT "The partial amino acid sequence of bovine cartilage proteoglycan,
RT deduced from a cDNA clone, contains numerous Ser-Gly sequences
RT arranged in homologous repeats.";
RL Biochem. J. 243:255-259(1987).
RN [4]
RP SEQUENCE OF 2114-2150 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=93352525; PubMed=8349621;
RA Fuelleop C., Walcz E., Valyon M., Glant T.T.;
RT "Expression of alternatively spliced epidermal growth factor-like
RT domains in aggrecans of different species. Evidence for a novel
RT module.";
RL J. Biol. Chem. 268:17377-17383(1993).
RN [5]
RP PARTIAL SEQUENCE.
RX MEDLINE=85027710; PubMed=6489519;
RA Perin J.-P., Bonnet F., Jolles J., Jolles P.;
RT "Sequence data concerning the protein core of the cartilage
RT proteoglycan monomers. Characterization of a sequence allowing the
RT synthesis of an oligonucleotide probe.";
RL FEBS Lett. 176:37-42(1984).
RN [6]
RP PARTIAL SEQUENCE.
RX MEDLINE=87005253; PubMed=3530809;
RA Perin J.P., Bonnet F., Jolles P.;
RT "Structural relationship between link proteins and proteoglycan
RT monomers.";
RL FEBS Lett. 206:73-77(1986).
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
CC matrix of cartilaginous tissues. A major function of this protein
CC is to resist compression in cartilage. It binds avidly to
CC hyaluronic acid via an amino-terminal globular region. May play a
CC regulatory role in the matrix assembly of the cartilage.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P13608-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P13608-2; Sequence=VSP_003072;
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
CC terminus of the proteoglycan, while another globular region, G3,
CC makes up the C-terminus. G1 contains link domains and thus
CC consists of three disulfide-bonded loop structures designated as
CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
CC and the chondroitin sulfate (CS) attachment domains lie between G2
CC and G3.
CC -!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-
CC LINKED (ABOUT 40) OLIGOSACCHARIDES.
CC -!- PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN
CC ADULT AND FETAL BOVINE PROTEOGLYCANS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
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CC -----
DR EMBL; U76615; AAB38524.1; --
DR EMBL; L07053; --; NOT_ANNOTATED_CDS.
DR PIR; A34234; A39808.
DR PIR; T42630; T42630.
DR HSSP; P08709; 1BF9.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR000152; Asx_hydroxyl_s.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR003324; SGXSG.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF02339; SGXSG; 61.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; xlink; 4.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 4.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00445; LINK; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
DR PROSITE; PS01241; LINK; 4.
KW Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
KW Calcium; Alternative splicing; Repeat; Immunoglobulin domain.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 2364 AGGREGAN CORE PROTEIN.
FT DOMAIN 25 147 IG-LIKE V-TYPE.
FT DOMAIN 170 247 LINK 1.
FT DOMAIN 268 349 LINK 2.
FT DOMAIN 504 581 LINK 3.
FT DOMAIN 602 683 LINK 4.
FT DOMAIN 774 907 23 X 6 AA APPROXIMATE TANDEM REPEATS OF
```


FT DOMAIN 1433 2112 E-[EX]-P-F-P-S.
FT DOMAIN 2113 2149 CS-2.
FT DOMAIN 2114 2364 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2161 2276 G3.
FT DOMAIN 2280 2338 C-TYPE LECTIN.
FT DISULFID 51 133 SUSHI.
FT DISULFID 175 246 BY SIMILARITY.
FT DISULFID 199 220 BY SIMILARITY.
FT DISULFID 273 348 BY SIMILARITY.
FT DISULFID 297 318 BY SIMILARITY.
FT DISULFID 509 580 BY SIMILARITY.
FT DISULFID 533 554 BY SIMILARITY.
FT DISULFID 607 682 BY SIMILARITY.
FT DISULFID 631 652 BY SIMILARITY.
FT DISULFID 2117 2128 BY SIMILARITY.
FT DISULFID 2182 2274 BY SIMILARITY.
FT DISULFID 2250 2266 BY SIMILARITY.
FT DISULFID 2281 2324 BY SIMILARITY.
FT DISULFID 2310 2337 BY SIMILARITY.
FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 667 667 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 2114 2150 Missing (in isoform 2).
FT SEQUENCE 2364 AA; 246359 MW; 6FF83763420C3D4C CRC64;
FT Query Match 14.3%; Score 158.5; DB 1; Length 2364;
FT Best Local Similarity 26.8%; Pred. No. 7.4e-06;
FT Matches 48; Conservative 29; Mismatches 59; Indels 43; Gaps 10;
QY 7 QPVCRGG---TORPCYKVIYFHDTSRRLLNFEEAKEACRRDGGQLVLSIESDEQKLEKFI 63
Db 2151 QKLCBEGWTKFQGHCHYR--HPPD---RATWVDAESQCRKQSHLSSIVTPEEQ----EFV 2201
QY 64 ENLLPSDGDFF-WIGLRRREBKQNSTACQDLYAWTDGSIQFRNYYVDEP----SCGSEV 118
Db 2202 NN---NAQDYQWIGL-----NDKTIEGDFRWSGDGSHSLQFENWRPNQPDNFFATGEDC 2250
QY 119 CVVMYHQPSAPAGIGGYPVFWQNDRCNMKNFNICKYS----DEKPAVPSREAEGEETE 173
Db 2251 VVMWHEKG-----EWNDFVPCNYQLPFTCKRGTVACGEPVVEHARIFGQKXD 2298
RESULT 14
PGCA_HUMAN STANDARD; PRT; 2415 AA.
ID PGCA_HUMAN STANDARD; PRT; 2415 AA.
AC P16112; Q13650;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPC) (Chondroitin sulfate proteoglycan core protein 1).
GN AGC1 OR CSPG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Chondrocytes;
RX MEDLINE=91093289; PubMed=1985970;
RA Doegi K.J., Sasaki M., Kimura T., Yamada Y.;
RT "Complete coding sequence and deduced primary structure of the human
RT cartilage large aggregating proteoglycan, aggrecan. Human-specific
RT repeats, and additional alternatively spliced forms.";
RL J. Biol. Chem. 266:894-902(1991).
RN [2]
RP SEQUENCE OF 1778-2415 FROM N.A. (ISOFORM 2).
RC TISSUE=Chondrocytes;

RA Dudhia J., Hardingham T.E.;
RL Submitted (JAN-1990) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1936-2415 FROM N.A. (ISOFORM 1).
RX MEDLINE=89380154; PubMed=2789216;
RA Baldwin C.T., Reginato A.M., Prockop D.J.;
RT "A new epidermal growth factor-like domain in the human core protein
RT for the large cartilage-specific proteoglycan. Evidence for
RT alternative splicing of the domain.";
RL J. Biol. Chem. 264:15747-15750(1989).
RN [4]
RP SEQUENCE OF 764-864 FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95128522; PubMed=7827755;
RA Barry F.P., Neame P.J., Sasse J., Pearson D.;
RT "Length variation in the keratan sulfate domain of mammalian
RT aggrecan.";
RL Matrix Biol. 14:323-328(1994).
CC -!- FUNCTION: THIS PROTEOGLYCAN IS A MAJOR COMPONENT OF EXTRACELLULAR
CC MATRIX OF CARTILAGINOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN
CC IS TO RESIST COMPRESSION IN CARTILAGE. IT BINDS AVIDLY TO
CC HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR REGION.
CC -!- SUBUNIT: Interacts with FBLN1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1; IsoId=P16112-1; Sequence=Displayed;
CC Name=2; IsoId=P16112-2; Sequence=VSP_003074;
CC Name=3; IsoId=P16112-3; Sequence=VSP_003074, VSP_003075;
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
CC terminus of the proteoglycan, while another globular region, G3,
CC makes up the COOH terminus. G1 contains link domains and thus
CC consists of three disulfide-bonded loop structures designated as
CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
CC and the chondroitin sulfate (CS) attachment domains lie between G2
CC and G3.
CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate
CC chains, N-linked and O-linked oligosaccharides.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M55172; AAA62824.1; -;
CC EMBL; J05062; AAA35726.1; -;
CC EMBL; X17406; CAA35463.1; -;
CC EMBL; S74659; AAC60643.2; -;
CC PIR; A39086; A39086.
CC HSSP; P98066; ITSG.
CC Genew; HGNC:319; AGC1.
CC MIM; 155760; -;
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.

regulatory role in the matrix assembly of the cartilage.
 -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).
 -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino terminus of the proteoglycan, while another globular region, G3, makes up the COOH terminus. G1 contains link domains and thus consists of three disulfide-bonded loop structures designated as the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS) and the chondroitin sulfate (CS) attachment domains lie between G2 and G3.
 -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate chains, N-linked and O-linked oligosaccharides (By similarity).
 -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 -!- SIMILARITY: Contains 4 link domains.
 -!- SIMILARITY: Contains 1 C-type lectin family domain.
 -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 -!- SIMILARITY: Contains 1 EGF-like domain.
 -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

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EMBL; U65989; AAB06238.2; -.
 EMBL; S74662; AAC60527.1; -.
 EMBL; L07054; -; NOT_ANNOTATED_CDS.
 PIR; I46998; I46998.
 HSP; P08709; I46998.
 InterPro; IPR002353; AntifreezeII.
 InterPro; IPR000152; Asx hydroxyl_s.
 InterPro; IPR000742; EGF_2.
 InterPro; IPR001881; EGF_CA.
 InterPro; IPR006209; EGF-like.
 InterPro; IPR007110; Ig-like.
 InterPro; IPR003006; Ig_MHC.
 InterPro; IPR001304; Lectin_C.
 InterPro; IPR000538; Link.
 InterPro; IPR003324; SGXSG.
 InterPro; IPR000436; Sushi_SCR_CCP.
 Pfam; PF00008; EGF; 1.
 Pfam; PF00047; ig; 1.
 Pfam; PF00059; lectin_c; 1.
 Pfam; PF02339; SGXSG; 66.
 Pfam; PF00084; sushi; 1.
 Pfam; PF00193; Xlink; 4.
 PRINTS; PR00356; ANTIFREEZEII.
 PRINTS; PR01265; LINKMODULE.
 ProDom; PD00918; Link; 4.
 SMART; SM00032; CCP; 1.
 SMART; SM00034; CLECT; 1.
 SMART; SM00179; EGF_CA; 1.
 SMART; SM00445; LINK; 4.
 PROSITE; PS00010; ASX HYDROXYL; 1.
 PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 PROSITE; PS00041; C-TYPE LECTIN_2; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS01835; IG LIKE; 1.
 PROSITE; PS00290; IG_MHC; 1.
 PROSITE; PS01241; LINK; 4.
 Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain; Repeat; Immunoglobulin domain.
 SIGNAL; 1 16 POTENTIAL.
 CHAIN; 17 2333 AGGECAN CORE PROTEIN.
 DOMAIN; 34 147 IG-LIKE V-TYPE.
 DOMAIN; 170 247 LINK 1.
 DOMAIN; 268 349 LINK 2.
 DOMAIN; 513 590 LINK 3.

FT	DOMAIN	611	692	LINK 4.
FT	DOMAIN	2081	2117	EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	2130	2245	C-TYPE LECTIN.
FT	DOMAIN	2249	2307	SUSHI.
FT	DOMAIN	48	140	G1-A.
FT	DOMAIN	152	247	G1-B.
FT	DOMAIN	253	349	G1-B'.
FT	DOMAIN	495	589	G2-B.
FT	DOMAIN	596	691	G2-B'.
FT	DOMAIN	694	816	KS.
FT	DOMAIN	819	1394	CS-1.
FT	DOMAIN	1395	2079	CS-2.
FT	DOMAIN	2080	2333	G3.
FT	DISULFID	51	133	BY SIMILARITY.
FT	DISULFID	175	246	BY SIMILARITY.
FT	DISULFID	199	220	BY SIMILARITY.
FT	DISULFID	273	348	BY SIMILARITY.
FT	DISULFID	297	318	BY SIMILARITY.
FT	DISULFID	518	589	BY SIMILARITY.
FT	DISULFID	542	563	BY SIMILARITY.
FT	DISULFID	616	691	BY SIMILARITY.
FT	DISULFID	640	661	BY SIMILARITY.
FT	DISULFID	2085	2096	BY SIMILARITY.
FT	DISULFID	2090	2105	BY SIMILARITY.
FT	DISULFID	2107	2116	BY SIMILARITY.
FT	DISULFID	2123	2134	BY SIMILARITY.
FT	DISULFID	2151	2243	BY SIMILARITY.
FT	DISULFID	2219	2235	BY SIMILARITY.
FT	DISULFID	2250	2293	BY SIMILARITY.
FT	DISULFID	2279	2306	BY SIMILARITY.
FT	CARBOHYD	126	126	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	333	333	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	387	387	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	444	444	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	620	620	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	676	676	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	747	747	N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	2333 AA;	240573 MW;	8B9ED78F3508B596 CRC64;
Query Match				
Best Local Similarity				
Matches				
Score 155.5; DB 1; Length 2333;				
Pred. No. 1.3e-05;				
Conservative 24; Mismatches 61; Indels 43; Gaps 11;				
QY	7 QVCEGG---	TQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLEKFI	63	
Db	2120 QELCEEGTWFQGHGCHYR--YFPD---	RESWVDAESRCRAQQSHLSIVTPEEQ----	EFV	2170
QY	64 ENLLPSDGF-WIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS---	CGSEVC	119	
Db	2171 NN---NAQDYQWIGL-----	NDRTIEGDFRWSGDHSLQFENWRPNQPDNFFVSGDC	2219	
QY	120 VVM-YHQPAPAGIGGYPYFQWDDRCNMKNFKYKYS----	DEKPAVPSRAEGETE	173	
Db	2220 VVMTWHEKG-----	EWNDVPCNYLPTCKKGTACGDPVVEHARTFGQKGD	2267	
RESULT 16				
LEM2_MOUSE				
ID	LEM2_MOUSE	STANDARD;	PRT;	612 AA.
AC	Q00690;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	E-selectin precursor (Endothelial leukocyte adhesion molecule 1)			
DE	(ELAM-1) (Leukocyte-endothelial cell adhesion molecule 2) (LECAM2)			
GN	SELE OR ELAM-1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

Immunity 10:691-700(1999).

[3]

SEQUENCE FROM N.A.

STRAIN=129/SV; TISSUE=Endothelial cells, and Spleen;

MEDLINE=93359842; PubMed=10430665;

Norsworthy P.J., Taylor P.R., Walport M.J., Botto M.;

"Cloning of the mouse homolog of the 126-kDa human C1q/MBL/SP-A receptor, C1qRp.";

Mamm. Genome 10:789-793(1999).

-!- FUNCTION: Receptor (or element of a larger receptor complex) for C1q, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in intercellular adhesion. Marker for early multipotent hematopoietic precursor cells. May play a role in cell-cell interactions during hematopoietic and vascular development.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Expressed in lung, heart and bone marrow. Expressed at lower level in ovary, whole embryo and fetal liver. Not detected in brain, adult liver or thymus. Highly expressed in peritoneal cavity and bone marrow macrophages. Not detected in epithelial cells.

-!- DEVELOPMENTAL STAGE: First detectable in day 9 embryos, in the endocardium and vascular endothelium in the anterior part of the embryo. Expression in endothelial cells, initially restricted to aorta, omphalomesenteric and umbilical arteries, later extends to subcardinal veins, intersomitic arteries and perimeural vessels. On day 10, detectable in the entire embryo.

-!- PTM: N- and O-glycosylated (By similarity).

-!- SIMILARITY: Contains 1 C-type lectin family domain.

-!- SIMILARITY: Contains 5 EGF-like domains.

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EMBL; AF074856; AAC63274.1; -.

EMBL; AF081789; AAC62649.1; -.

EMBL; AF099939; AAD47906.1; -.

EMBL; AF099938; AAD47906.1; JOINED.

HSSP; P35555; 1EMN.

MGD; MGI:106664; C1qr1.

GO; GO:0016023; C:cytoplasmic vesicle; IDA.

GO; GO:0016021; C:integral to membrane; ISS.

GO; GO:0005886; C:plasma membrane; IDA.

GO; GO:0004872; F:receptor activity; ISS.

GO; GO:0016337; P:cell-cell adhesion; ISS.

GO; GO:0042116; P:macrophage activation; ISS.

GO; GO:0006909; P:phagocytosis; ISS.

InterPro; IPR00152; Asx hydroxyl S.

InterPro; IPR01881; EGF_Ca.

InterPro; IPR006209; EGF_like.

InterPro; IPR01304; Lectin_C.

Pfam; PF00008; EGF; 5.

Pfam; PF00059; lectin_c; 1.

SMART; SM00034; CLECT; 1.

SMART; SM00179; EGF_CA; 3.

PROSITE; PS00010; ASX HYDROXYL; 3.

PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.

PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.

PROSITE; PS01186; EGF_2; 3.

PROSITE; PS50026; EGF_3; 4.

PROSITE; PS01187; EGF_CA; 3.

Cell adhesion; Receptor; Repeat; Signal; Transmembrane;

EGF-like domain; Lectin; Glycoprotein.

SIGNAL 1 22

CHAIN 23 644

DOMAIN 23 572

COMPLEMENT COMPONENT C1Q RECEPTOR.

EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	573	593	POTENTIAL.
FT	DOMAIN	594	644	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	31	173	C-TYPE LECTIN.
FT	DOMAIN	257	298	EGF-LIKE 1.
FT	DOMAIN	299	341	EGF-LIKE 2.
FT	DOMAIN	342	381	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	382	423	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	424	465	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DISULFID	261	272	BY SIMILARITY.
FT	DISULFID	268	282	BY SIMILARITY.
FT	DISULFID	284	297	BY SIMILARITY.
FT	DISULFID	303	314	BY SIMILARITY.
FT	DISULFID	308	325	BY SIMILARITY.
FT	DISULFID	327	340	BY SIMILARITY.
FT	DISULFID	346	355	BY SIMILARITY.
FT	DISULFID	351	364	BY SIMILARITY.
FT	DISULFID	366	380	BY SIMILARITY.
FT	DISULFID	386	397	BY SIMILARITY.
FT	DISULFID	393	406	BY SIMILARITY.
FT	DISULFID	408	422	BY SIMILARITY.
FT	DISULFID	428	440	BY SIMILARITY.
FT	DISULFID	436	449	BY SIMILARITY.
FT	DISULFID	451	464	BY SIMILARITY.
FT	CARBOHYD	102	102	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	322	322	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	644 AA;	69354 MW;	EB4351648BF8635A CRC64;

Query Match

13.9%; Score 153.5; DB 1; Length 644;

Best Local Similarity

24.1%; Pred. No. 4.1e-06;

Matches 51; Conservative 32; Mismatches 70; Indels 59; Gaps 11;

QY	4	LSGP	-----VCRGGTQPCYKVIYFHTSRRLNFEEAKEACRRDGGQLVSIES	52
Db	13	LLGPWAGAAADSQAVCEG	---TACYTAHW-----GKLSAAEAQHRCNENGNGNLATVKS	64
QY	53	EDEQKLEKFIENLLPSD	-----GDFWIGLRREKQSNSTACQDL-----YAWT-DGS	100
Db	65	EEEARHVQALTLQKTKAPLEAKMGKFWIGLQR	---EKGNCYHDLPLMRGFSWVGGE	120
QY	101	ISQFNWY-VDEPSCGSEVCVMV	-----HQPSAPAGIGGYPYMFQWDDRC-----	145
Db	121	DTAYSNWYKASKSSCIFKRCVSLDLSLTPHPHLP	-----KWHESFCGTPEAPG	171
QY	146	NMKNFICKYSDEKPAVPSREAEGETELTTP	177	
Db	172	NSIEGFLCKFNFKGMCRLALGGPGRVITYTTP	203	

RESULT 18

PGCA RAT

ID -PGCA RAT

STANDARD; PRT; 2124 AA.

AC P07897;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE AggreCan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).

DE AGC1 OR AGC.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN	[1]	SEQUENCE FROM N.A.		
RP	MEDLINE=8807070; PubMed=3693370;			
RX	Doerge K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.;			
RA	"Complete primary structure of the rat cartilage proteoglycan core protein deduced from cDNA clones.";			
RT	J. Biol. Chem. 262:17757-17767(1987).			
RL	[2]			
RP	REVISION TO 698.			
RA	Doerge K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.;			
RL	J. Biol. Chem. 263:10040-10040(1988).			

[3]
RN SEQUENCE OF 1856-2124 FROM N.A.
RP MEDLINE=86250698; PubMed=2424893;
RX Doerge K., Fernandez P., Hassell J.R., Sasaki M., Yamada Y.;
RA "Partial cDNA sequence encoding a globular domain at the C terminus
of the rat cartilage proteoglycan.";
RT J. Biol. Chem. 261:8108-8111(1986).
RL
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
matrix of cartilaginous tissues. A major function of this protein
is to resist compression in cartilage. It binds avidly to
hyaluronic acid via an amino-terminal globular region. May play a
regulatory role in the matrix assembly of the cartilage.
CC -!- SUBUNIT: Interacts with FBLN1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
similarity).
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
terminus of the proteoglycan, while another globular region, G3,
makes up the COOH terminus. G1 contains link domains and thus
consists of three disulfide-bonded loop structures designated as
the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
and the chondroitin sulfate (CS) attachment domains lie between G2
and G3.
CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate
chains, N-linked and O-linked oligosaccharides.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
or send an email to license@isb-sib.ch).

DR EMBL; M13518; AAA41836.1; --
DR EMBL; J03485; AAA21000.1; ALT_SEQ.
DR PIR; A92623; A28452.
DR HSSP; P98066; ITSG.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR003324; SGXSXG.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF02339; SGXSXG; 55.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; Xlink; 4.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 4.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00445; LINK; 4.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS01241; LINK; 4.
KW Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; Repeat;
KW Immunoglobulin domain.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 2124 AGGREGAN CORE PROTEIN.
FT DOMAIN 34 147 IG-LIKE V-TYPE.
FT DOMAIN 170 247 LINK 1.

FT DOMAIN 268 349 LINK 2.
FT DOMAIN 504 581 LINK 3.
FT DOMAIN 602 683 LINK 4.
FT DOMAIN 1910 2036 C-TYPE LECTIN.
FT DOMAIN 2040 2098 SUSHI.
FT DOMAIN 48 140 G1-A.
FT DOMAIN 152 247 G1-B.
FT DOMAIN 253 349 G1-B'.
FT DOMAIN 486 580 G2-B.
FT DOMAIN 587 682 G2-B'.
FT DOMAIN 685 798 KS.
FT DOMAIN 801 1226 CS-1.
FT DOMAIN 1227 1909 CS-2.
FT DOMAIN 1910 2124 G3.
FT DISULFID 51 133 BY SIMILARITY.
FT DISULFID 175 246 BY SIMILARITY.
FT DISULFID 199 220 BY SIMILARITY.
FT DISULFID 273 348 BY SIMILARITY.
FT DISULFID 297 318 BY SIMILARITY.
FT DISULFID 509 580 BY SIMILARITY.
FT DISULFID 533 554 BY SIMILARITY.
FT DISULFID 607 682 BY SIMILARITY.
FT DISULFID 631 652 BY SIMILARITY.
FT DISULFID 1914 1925 BY SIMILARITY.
FT DISULFID 1942 2034 BY SIMILARITY.
FT DISULFID 2010 2026 BY SIMILARITY.
FT DISULFID 2041 2084 BY SIMILARITY.
FT DISULFID 2070 2097 BY SIMILARITY.
FT CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 667 667 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1842 1842 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 2124 AA; 221117 MW; E30BBE61593A34B1 CRC64;

Query Match 13.9%; Score 153.5; DB 1; Length 2124;
Best Local Similarity 26.3%; Pred. No. 1.8e-05;
Matches 47; Conservative 27; Mismatches 62; Indels 43; Gaps 9;

QY 7 QPVCRRGG---TQRPCKYVIYFHDTSRLNFEAEAKEACRRDGGQLVSISEDEQKLIKFI 63
Db 1911 QEQCEEGWTKFQGHCYR--HFPP---RETWVDAERRCREQQSHLSIVTPEEQEFVNKNA 1965

QY 64 ENLLPSDGF-WIGLRRREKQSNSTACQDLVYAWTDGSIQFRNRYVDEP---SCGSEV 118
Db 1966 Q-----DYQWIGL-----NDRTIEGDFRWSDDGHSLSQFEKWRPNQPDNFFATGDC 2010

QY 119 CVVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFNICKYS---DEKPAVPSREAEGEETE 173
Db 2011 VVMIIWHERG-----EWNDVPCNYQLPFTCKKGTGACGPPAVEHARTLGQK 2058

RESULT 19
PGCB_BOVIN
ID PGCB_BOVIN STANDARD; PRT; 912 AA.
AC Q28062;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Brevican core protein precursor.
GN BCAN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94193597; PubMed=8144512;
RA Yamada H., Watanabe K., Shimonaka M., Yamaguchi Y.;


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CC      EMBL; U94333; AAB53110.1; -.
CC      EMBL; AL118508; CAC00597.1; -.
DR      EMBL; BC028075; AAH28075.1; -.
DR      HSSP; P35555; IEMN.
DR      Genew; HGNC:15855; C1QR1.
DR      MIM; 120577; -.
DR      GO; GO:0016021; C:integral to membrane; IC.
DR      GO; GO:0004872; F:receptor activity; NAS.
DR      GO; GO:0016337; P:cell-cell adhesion; IDA.
DR      GO; GO:0042116; P:macrophage activation; NAS.
DR      GO; GO:0006909; P:phagocytosis; NAS.
DR      InterPro; IPR000152; Asx_hydroxyl_S.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR006209; EGF_like.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00008; lectin_c; 1.
DR      Pfam; PF00059; lectin_c; 1.
DR      SMART; SM00034; CLECT; 1.
DR      SMART; SM00179; EGF_CA; 3.
DR      PROSITE; PS00010; ASX_HYDROXYL; 3.
DR      PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR      PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR      PROSITE; PS01186; EGF_2; 3.
DR      PROSITE; PS00026; EGF_3; 3.
DR      PROSITE; PS01187; EGF_CA; 3.
KW      Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
KW      EGF-like domain; Lectin; Glycoprotein; Polymorphism.
FT      SIGNAL          1   21
FT      CHAIN           22   652
FT      DOMAIN          24   580
FT      TRANSMEM        581   601
FT      DOMAIN          602   652
FT      DOMAIN          32   174
FT      DOMAIN          260   301
FT      DOMAIN          302   344
FT      DOMAIN          345   384
FT      DOMAIN          385   426
FT      DOMAIN          427   468
FT      DOMAIN          594   601
FT      DISULFID         264   275
FT      DISULFID         271   285
FT      DISULFID         287   300
FT      DISULFID         306   317
FT      DISULFID         311   328
FT      DISULFID         330   343
FT      DISULFID         349   358
FT      DISULFID         354   367
FT      DISULFID         369   383
FT      DISULFID         389   400
FT      DISULFID         396   409
FT      DISULFID         411   425
FT      DISULFID         431   443
FT      DISULFID         439   452
FT      DISULFID         454   467
FT      CARBOHYD        325   325
FT      VARIANT         318   318
FT      CONFLICT        22    22
FT      CONFLICT        36    36
FT      CONFLICT        38    39
FT      CONFLICT       155   155
FT      CONFLICT       186   186
FT      CONFLICT       492   492
FT      CONFLICT       496   496
FT      CONFLICT       504   504
FT      COMPLEMENT COMPONENT C1Q RECEPTOR.
FT      EXTRACELLULAR (POTENTIAL).
FT      POTENTIAL.
FT      CYTOPLASMIC (POTENTIAL).
FT      C-TYPE LECTIN.
FT      EGF-LIKE 1.
FT      EGF-LIKE 2.
FT      EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT      POLY-LEU.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      BY SIMILARITY.
FT      N-LINKED (GLCNAC... ) (POTENTIAL).
FT      V -> A.
FT      /FTid=VAR_013573.
FT      T -> V (IN REF. 1; AA SEQUENCE).
FT      C -> T (IN REF. 1; AA SEQUENCE).
FT      TA -> RI (IN REF. 1; AA SEQUENCE).
FT      S -> N (IN REF. 1).
FT      G -> A (IN REF. 1; AA SEQUENCE).
FT      S -> A (IN REF. 1; AA SEQUENCE).
FT      R -> Q (IN REF. 1; AA SEQUENCE).
FT      R -> G (IN REF. 1; AA SEQUENCE).
```

Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;

"The DNA sequence and comparative analysis of human chromosome 20.;" Nature 414:865-871 (2001).

[4]

SEQUENCE FROM N.A.

TISSUE=Leukocyte;

MEDLINE=2238257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;" Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[5]

CHARACTERIZATION.

MEDLINE=21990337; PubMed=11994479;

McGreal E.P., Ikewaki N., Akatsu H., Morgan B.P., Gasque P.;

"Human Clqrp is identical with CD93 and the mNI-11 antigen but does not bind Clq.;" J. Immunol. 168:5222-5232 (2002).

[6]

O-GLYCOSYLATION.

MEDLINE=99192777; PubMed=10092817;

Nepomuceno R.R., Ruiz S., Park M., Tenner A.J.;

"Clqrp is a heavily O-glycosylated cell surface protein involved in the regulation of phagocytic activity.;" J. Immunol. 162:3583-3589 (1999).

-!- FUNCTION: Receptor (or element of a larger receptor complex) for Clq, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in intercellular adhesion.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Highly expressed in endothelial cells, platelets, cells of myeloid origin, such as monocytes and neutrophils. Not expressed in cells of lymphoid origin.

-!- PTM: N- and O-glycosylated.

-!- SIMILARITY: Contains 1 C-type lectin family domain.

-!- SIMILARITY: Contains 5 EGF-like domains.

-!- CAUTION: Has been sometimes referred to as a collectin receptor.

-!- CAUTION: According to Ref.5, Clq is not a ligand for ClqR1.

-!- DATABASE: NAME=PROW; NOTE=PROW 3:1-6(2001); WWW="http://www.ncbi.nlm.nih.gov/prow/guide/467246456_g.htm".

FT CONFLICT 541 541 P -> S (IN REF. 1).
SQ SEQUENCE 652 AA; 68560 MW; EECA0FEAC55FCAC2 CRC64;

Query Match 13.7%; Score 151.5; DB 1; Length 652;
Best Local Similarity 24.4%; Pred. No. 6.4e-06;
Matches 50; Conservative 38; Mismatches 74; Indels 43; Gaps 9;

QY 3 LLSGQF-----VCRGQTQPCYKVIYFHDTSRRRLNFEEAKEACRRDGGQLVSIE 51
DB 13 LLLTQPGAGTGADTEAVCVG---TACYTA-----HSGKLSAAEAQNHQNGNLTATVK 64

QY 52 SEDEOKLIEKFIENLLPSD-----GDFWIGLRRREKQSNSTACQDLYAWT-DGSISQ 103
DB 65 SKEBAQHVRVLAQLLRREALTARMSKFWIGLQREKGLDPSLPKGFWSVGGGEDTP 124

QY 104 FRNWDYD-EPSCGSEVCVVM---YHQPAPAGIGGPFYQWDDRCNMKN-----FI 152
DB 125 YSNWHKELRNSCISKRCVSLDLLDLSQPLPSRLP-----KWSEGPGSGSPGSNIEGFV 179

QY 153 CKYSDEKPAVPSREAEGETELTTP 177
DB 180 CKFSFKGMCRLALGGPGQVYTTTP 204

RESULT 21
CLE1_HUMAN
ID CLE1_HUMAN STANDARD; PRT; 197 AA.
AC 075596;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-type lectin superfamily member 1 precursor (Cartilage-derived C-type lectin).
GN CLECSF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=99453719; PubMed=10524194;
RA Neame P.J., Tapp H., Grimm D.R.;
RT "The cartilage-derived, C-type lectin (CLECSF1): structure of the gene and chromosomal location."
RL Biochim. Biophys. Acta 1446:193-202(1999).
CC -!- TISSUE SPECIFICITY: Restricted to cartilage.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
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CC -----
DR EMBL; AF077345; AAD12542.1; -.
DR EMBL; AF077344; AAD12542.1; JOINED.
DR HSSP; P05452; 1HTN.
DR Genew; HGNC:2052; CLECSF1.
DR GO; GO:0005530; F:lectin; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 197 C-TYPE LECTIN SUPERFAMILY MEMBER 1.
FT DOMAIN 74 192 C-TYPE LECTIN

FT DISULFID 95 191 BY SIMILARITY.
FT DISULFID 167 183 BY SIMILARITY.
SQ SEQUENCE 197 AA; 22232 MW; BB924DBDD7729A4 CRC64;

Query Match 13.7%; Score 151; DB 1; Length 197;
Best Local Similarity 25.0%; Pred. No. 1.6e-06;
Matches 38; Conservative 26; Mismatches 64; Indels 24; Gaps 4;

QY 7 QPVCRGQTQ--RPGYKVIYFHDTSRRRLNFEEAKEACRRDGGQLVSIESEDEOKLIEKFIE 64
DB 65 QTVCLRGTKVHKCYLA-----SEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGK 119

QY 65 NLLPSDGDGFWIGLRRREKQSNSTACQDLYAWTDSISQFRNWDYDEPSCGSEVCVVMYH 124
DB 120 RSLPGVNDFWLGI-----NDMVTGKFDVNVGIAISFLNWDRAQPNKGKRENCVLFS 171

QY 125 QPSAPAGIGGPFYQWDDRCNMKNFICKYS 156
DB 172 QSA-----QGKWSDEACRSKRYICEFT 194

RESULT 22
FCE2_HUMAN
ID FCE2_HUMAN STANDARD; PRT; 321 AA.
AC P06734;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Low affinity immunoglobulin epsilon FC receptor (Lymphocyte IgE receptor) (FC-epsilon-RII) (CD23) (BLAST-2) (Immunoglobulin E-binding factor).
DE factor).
GN FCER2 OR IGEBF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87118255; PubMed=2949326;
RA Ikuta K., Takami M., Kim C.W., Honjo T., Miyoshi T., Tagaya Y., Kawabe T., Yodoi J.;
RT "Human lymphocyte Fc receptor for IgE: sequence homology of its cloned cDNA with animal lectins."
RL Proc. Natl. Acad. Sci. U.S.A. 84:819-823(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87051737; PubMed=28777743;
RA Kikutani H., Inui S., Sato R., Barsumian E.L., Owaki H., Yamasaki K., Kaisho T., Uchibayashi N., Hardy R.R., Hirano T., Tsunawasa S., Sakiyama F., Suemura M., Kishimoto T.;
RT "Molecular structure of human lymphocyte receptor for immunoglobulin E";
RL Cell 47:657-665(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218454; PubMed=3034567;
RA Luedin C., Hofstetter H., Sarfati M., Levy C.A., Suter U., Alaimo D., Kilchherr E., Frost H., Delespesse G.;
RT "Cloning and expression of the cDNA coding for a human lymphocyte IgE receptor";
RL EMBO J. 6:109-114(1987).
RN [4]
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=93038513; PubMed=1417742;
RA Rose K., Turcatti G., Graber P., Pochon S., Regamey P.-O., Jansen K.U., Magnenat E., Aubonne N., Bonnefoy J.-Y.;
RT "Partial characterization of natural and recombinant human soluble CD23";
RL Biochem. J. 286:819-824(1992).
RN [5]
RP ALTERNATIVE SPLICING.
RX MEDLINE=89028672; PubMed=2972386;

RA Suemura M., Kishimoto T.;
RT "Two species of human Fc epsilon receptor II (Fc epsilon RII/CD23):
RL tissue-specific and IL-4-specific regulation of gene expression.";
RN Cell 55:611-618(1988).
RP [6]
RX 3D-STRUCTURE MODELING OF LECTIN DOMAIN.
RA MEDLINE=94191542; PubMed=8142907;
RA Padlan E.A., Helm B.A.;
RT "Modeling of the lectin-homology domains of the human and murine low-
RT affinity Fc epsilon receptor (Fc epsilon RII/CD23).";
RL Receptor 3:325-341(1993).
RN [7]
RP 3D-STRUCTURE MODELING OF 173-285.
RX MEDLINE=96276216; PubMed=8745401;
RA Bajorath J., Aruffo A.;
RT "Structure-based modeling of the ligand binding domain of the human
RT cell surface receptor CD23 and comparison of two independently
RT derived molecular models.";
RL Protein Sci. 5:240-247(1996).
CC -!- FUNCTION: This receptor has essential roles in the regulation of
CC IGE production and in the differentiation of B-cells (it is a B-
CC cell-specific antigen).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS A
CC SOLUBLE EXCRETED FORM.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P06734-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P06734-2; Sequence=VSP_003057;
CC -!- PTM: N- and O-glycosylated.
CC -!- MISCELLANEOUS: There are two kinds of Fc receptors for IGE, which
CC differ in both structure and function: high affinity receptors on
CC basophils and mast cells and low affinity receptors on lymphocytes
CC and monocytes.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD23 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd23.htm".
CC -----
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CC -----
DR EMBL; M15059; AAA52434.1; -;
DR EMBL; M14766; AAA52435.1; -;
DR EMBL; X04772; CAA28465.1; -;
DR EMBL; M23562; AAA52433.1; -;
DR PIR; A26067; LNHUER.
DR PDB; 1HLI; 31-JAN-94.
DR PDB; 1KJE; 03-APR-96.
DR Genew; HGNC:3612; FCER2.
DR MIM; 151445; -;
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0005178; F: integrin binding; TAS.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor; Antigen; IGE-binding protein; Repeat; Signal-anchor;
KW Transmembrane; Lectin; Glycoprotein; Alternative splicing;
KW 3D-structure.
FT CHAIN 1 321 MEMBRANE BOUND FORM.
FT CHAIN 150 321 SOLUBLE FORM.
FT DOMAIN 1 21 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 22 47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).

FT DOMAIN 48 321 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 162 284 C-TYPE LECTIN (LONG FORM).
FT SITE 149 150 CLEAVAGE.
FT REPEAT 69 89
FT REPEAT 90 110
FT REPEAT 111 131
FT DISULFID 160 288
FT DISULFID 163 174
FT DISULFID 191 282
FT DISULFID 259 273
FT CARBOHYD 63 63
FT VARSPLIC 1 7
FT FT
FT CONFLICT 269 269
FT STRAND 174 177
FT HELIX 184 193
FT TURN 194 195
FT STRAND 197 198
FT HELIX 204 214
FT TURN 215 216
FT STRAND 219 228
FT STRAND 229 230
FT STRAND 231 234
FT TURN 235 236
FT STRAND 239 239
FT STRAND 245 245
FT TURN 247 248
FT TURN 254 255
FT STRAND 259 262
FT STRAND 264 265
FT STRAND 268 271
FT TURN 273 274
FT STRAND 281 284
SQ SEQUENCE 321 AA; 36468 MW; F86708C0E6515B87 CRC64;
Query Match 13.5%; Score 149; DB 1; Length 321;
Best Local Similarity 30.2%; Pred. No. 4.5e-06;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;
QY 15 QRPCYKVIYFHDTSRRLNFEAKACRRDGGQLVSIIESEDEQKLIKFIENLLPSDGDWF 74
Db 171 QRKCY---YFGKGTQK--WVHARYACDDMEGQLVSIHSPEDFLTKH-----ASHTGSW 220
QY 75 IGLRREEKQSNSTACQDLVATWDGSGISQFRNWIYVDEPSCGS--EVCVVMYHQPSAPAGI 132
Db 221 IGLRNLDLKGE-----FIWVDGSHVDYSNWAFCPTSRSQGDCVMM-----RGS 265
QY 133 GGPYMFQWDDRCNMK--NNFICKYSDEKPAV---PSREAGE-----ETELTPV 179
Db 266 G-----RWNDAFCDRLKLGAWVC-----DRLATCTPPASEGSAESMGPSRDPDGRLLPTPS 316
QY 179 LP 180
Db 317 AP 318
RESULT 23
PGCA MOUSE
ID PGCA MOUSE STANDARD; PRT; 2132 AA.
AC Q61282; Q64021;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
DE protein) (CSPCP).
DE AGC1 OR AGC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Cartilage;

RA MEDLINE=95104847; PubMed=7806222;
 RA Walcz E., Deak F., Erhardt P., Coulter S.N., Fueleop C., Horvath P.,
 RA Doege K.J., Glant T.T.;
 RT "Complete coding sequence, deduced primary structure, chromosomal
 RT localization, and structural analysis of murine aggrecan.";
 RL Genomics 22:364-371(1994).
 RN [2]
 RP SEQUENCE OF 211-326 FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=95004579; PubMed=7920633;
 RA Watanabe H., Kimata K., Line S., Strong D., Gao L.-Y., Kozak C.A.,
 RA Yamada Y.;
 RT "Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in
 RT the aggrecan gene.";
 RL Nat. Genet. 7:154-157(1994).
 RN [3]
 RP INTERACTION WITH FBLN1.
 RX MEDLINE=99329059; PubMed=10400671;
 RA Aspberg A., Adam S., Kostka G., Timpl R., Heinegaard D.;
 RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
 RT versican.";
 RL J. Biol. Chem. 274:20444-20449(1999).
 CC -!- FUNCTION: This proteoglycan is a major component of extracellular
 CC matrix of cartilaginous tissues. A major function of this protein
 CC is to resist compression in cartilage. It binds avidly to
 CC hyaluronic acid via an amino-terminal globular region. May play a
 CC regulatory role in the matrix assembly of the cartilage.
 CC -!- SUBUNIT: Interacts with FBLN1.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
 CC terminus of the proteoglycan, while another globular region, G3,
 CC makes up the COOH terminus. G1 contains link domains and thus
 CC consists of three disulfide-bonded loop structures designated as
 CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
 CC and the chondroitin sulfate (CS) attachment domains lie between G2
 CC and G3.
 CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate
 CC chains, N-linked and O-linked oligosaccharides.
 CC -!- DISEASE: Defects in AGC1 are the cause of cartilage matrix
 CC deficiency (CMD). CMD is an autosomal recessive syndrome
 CC characterized by cleft palate, short limbs, tail and snout.
 CC Mutation in strain CMD causes absence of aggrecan by truncation of
 CC the protein (mutation in the G1 domain).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 4 link domains.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L07049; AAC37670.1; -;
 DR EMBL; S73722; AAB32160.1; -;
 DR EMBL; S73721; AAB32160.1; JOINED.
 DR FIR; A55182; A55182.
 DR HSSP; P98066; 1TSG.
 DR MGD; MGI:99602; Agcl.
 DR InterPro; IPR002353; AntifreezeII.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR000538; Link.
 DR InterPro; IPR003324; SGXSG.
 DR InterPro; IPR000436; Sushi_SCR_CCP.

DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00059; lectin_c; 1.
 DR Pfam; PF02339; SCXSG; 60.
 DR Pfam; PF00084; sushi; 1.
 DR Pfam; PF00193; Xlink; 4.
 DR PRINTS; PR00356; ANTIFREEZEII.
 DR PRINTS; PR01265; LINKMODULE.
 DR ProDom; PD000918; Link; 4.
 DR SMART; SM00032; CCP; 1.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00445; LINK; 4.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PROSITE; PS01241; LINK; 4.
 KW Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; Repeat;
 KW Immunoglobulin domain.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 2132 AGGREGAN CORE PROTEIN.
 FT DOMAIN 34 147 IG-LIKE V-TYPE.
 FT DOMAIN 170 247 LINK 1.
 FT DOMAIN 268 349 LINK 2.
 FT DOMAIN 504 581 LINK 3.
 FT DOMAIN 602 683 LINK 4.
 FT DOMAIN 1918 2044 C-TYPE LECTIN.
 FT DOMAIN 2048 2106 SUSHI.
 FT DOMAIN 48 140 G1-A.
 FT DOMAIN 152 247 G1-B.
 FT DOMAIN 253 349 G1-B'.
 FT DOMAIN 486 580 G2-B.
 FT DOMAIN 587 682 G2-B'.
 FT DOMAIN 805 803 KS.
 FT DOMAIN 1231 1231 CS-1.
 FT DOMAIN 1232 1917 CS-2.
 FT DOMAIN 1917 2132 G3.
 FT DISULFID 51 133 BY SIMILARITY.
 FT DISULFID 175 246 BY SIMILARITY.
 FT DISULFID 199 220 BY SIMILARITY.
 FT DISULFID 273 348 BY SIMILARITY.
 FT DISULFID 297 318 BY SIMILARITY.
 FT DISULFID 509 580 BY SIMILARITY.
 FT DISULFID 533 554 BY SIMILARITY.
 FT DISULFID 607 682 BY SIMILARITY.
 FT DISULFID 631 652 BY SIMILARITY.
 FT DISULFID 1922 1933 BY SIMILARITY.
 FT DISULFID 1950 2042 BY SIMILARITY.
 FT DISULFID 2018 2034 BY SIMILARITY.
 FT DISULFID 2049 2092 BY SIMILARITY.
 FT DISULFID 2078 2105 BY SIMILARITY.
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 667 667 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1675 1675 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 1171 1173 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 2132 AA; 222008 MW; 0B2BCDFC6CDBA163 CRC64;

Query Match 13.3%; Score 147.5; DB 1; Length 2132;
 Best Local Similarity 24.7%; Pred. No. 6.3e-05;
 Matches 45; Conservative 30; Mismatches 64; Indels 43; Gaps 9;
 QY 4 LSGQPVCRGG---TQPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSESEDEQKLE 60
 Db 1916 VADQEQCEGWTQFGHCYR--HFPD---RETWVDAERRCRBQQSHLSSIVTPEEQEFVN 1970
 QY 61 KFIENLLPSDGDFF-WIGLRRRREKQSNSTACQDLYAWTDGSGISQFRNWYVDEP---SCG 115
 Db 1971 KNAQ-----DYQWIGL-----NDRITGDFRWSGDGHSLOFEKWRPNQPNFFATG 2015

ProDom; PD000918; Link; 2.
 DR SMART; SM00032; CCP; 1.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00445; LINK; 2.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PROSITE; PS01241; LINK; 2.
 DR Glycoprotein; Hyaluronic acid; Proteoglycan; Lectin; Signal; Sushi;
 KW EGF-like domain; Repeat; Immunoglobulin domain.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 883 BREVICAN CORE PROTEIN.
 FT DOMAIN 35 154 IG-LIKE V-TYPE.
 FT DOMAIN 173 250 LINK 1.
 FT DOMAIN 271 352 LINK 2.
 FT DOMAIN 622 658 EGF-LIKE.
 FT DOMAIN 658 786 C-TYPE LECTIN.
 FT DOMAIN 787 851 SUSHI.
 FT DISULFID 56 136 BY SIMILARITY.
 FT DISULFID 178 249 BY SIMILARITY.
 FT DISULFID 202 223 BY SIMILARITY.
 FT DISULFID 276 351 BY SIMILARITY.
 FT DISULFID 300 321 BY SIMILARITY.
 FT DISULFID 626 637 BY SIMILARITY.
 FT DISULFID 631 646 BY SIMILARITY.
 FT DISULFID 648 657 BY SIMILARITY.
 FT DISULFID 664 675 BY SIMILARITY.
 FT DISULFID 692 784 BY SIMILARITY.
 FT DISULFID 760 776 BY SIMILARITY.
 FT DISULFID 791 834 BY SIMILARITY.
 FT DISULFID 820 847 BY SIMILARITY.
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 883 AA; 96013 MW; CC2C33C97B453E45 CRC64;
 Query Match 13.3%; Score 147; DB 1; Length 883;
 Best Local Similarity 29.7%; Pred. No. 2.4e-05;
 Matches 43; Conservative 21; Mismatches 45; Indels 36; Gaps 8;
 QY 15 QRPCYKVIYFHTSRRLNFEAEKACRRDGGQLVSISEDEQKLI-EKFIEIENLLPSDGF 73
 Db 672 QGACYK---HFSTR-SWEEAESQCRALGAHLTSICTPEEQDFVNDRYREYQ----- 719
 QY 74 WIGLRRREKQSNSTACOLYAWTDGSIQFRNWYVDEPS---CGSEVCVVM-YHQPSAP 129
 Db 720 WIGL-----NDRTIEGDFLWSDGAPLLYENWNPQPDYSFLSGENCVMVWHDQG-- 769
 QY 130 AGIGGPYMFQWNNDRRCNMKNFICK 154
 Db 770 -----QWSDVPCNVHLSYTCK 785
 RESULT 25
 PGCA_CHICK
 ID PGCA_CHICK STANDARD; PRT; 2109 AA.
 AC P07898; Q90810; Q90820; Q90991; Q91047;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
 DE protein) (CSPCP).
 GN AGC1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;

RN [1] SEQUENCE FROM N.A.
RP STRAIN=White leghorn; TISSUE=Embryo;
RC MEDLINE=94043149; PubMed=8226878;
RX Li H., Schwartz N.B., Vertel B.M.;
RA "cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core
RT protein and identification of a stop codon in the aggrecan gene
RT associated with the chondrodystrophy, nanomelia.";
RL J. Biol. Chem. 268:23504-23511(1993).
RN [2]
RP SEQUENCE OF 1042-1559 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=90307744; PubMed=1694853;
RA Krueger R.C. Jr., Fields T.A., Mensch J.R. Jr., Schwartz N.B.;
RT "Chick cartilage chondroitin sulfate proteoglycan core protein. II.
RT Nucleotide sequence of cDNA clone and localization of the S103L
RT epitope.";
RL J. Biol. Chem. 265:12088-12097(1990).
RN [3]
RP SEQUENCE OF 1-1855 AND 1893-2109 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=93111968; PubMed=1339285;
RA Chandrasekaran L., Tanzer M.L.;
RT "Molecular cloning of chicken aggrecan. Structural analyses.";
RL Biochem. J. 288:903-910(1992).
RN [4]
RP ERRATUM.
RX MEDLINE=94107258; PubMed=8280087;
RA Chandrasekaran L., Tanzer M.L.;
RL Biochem. J. 296:885-887(1993).
RN [5]
RP SEQUENCE OF 1492-1610 FROM N.A.
RC STRAIN=White leghorn; TISSUE=Chondrocytes;
RX MEDLINE=95128519; PubMed=7827752;
RA Primorac D., Stover M.L., Clark S.H., Rowe D.W.;
RT "Molecular basis of nanomelia, a heritable chondrodystrophy of
RT chicken.";
RL Matrix Biol. 14:297-305(1994).
RN [6]
RP SEQUENCE OF 1894-2109 FROM N.A.
RX MEDLINE=89008500; PubMed=3170613;
RA Tanaka T., Har-El R., Tanzer M.L.;
RT "Partial structure of the gene for chicken cartilage proteoglycan
RT core protein.";
RL J. Biol. Chem. 263:15831-15835(1988).
RN [7]
RP SEQUENCE OF 1693-1855 AND 1893-2109 FROM N.A.
RX MEDLINE=86259736; PubMed=3460082;
RA Sai S., Tanaka T., Koshier R.A., Tanzer M.L.;
RT "Cloning and sequence analysis of a partial cDNA for chicken
RT cartilage proteoglycan core protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5081-5085(1986).
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
CC matrix of cartilaginous tissues. A major function of this protein
CC is to resist compression in cartilage. It binds avidly to
CC hyaluronic acid via an amino-terminal globular region. May play a
CC regulatory role in the matrix assembly of the cartilage.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P07898-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P07898-2; Sequence=VSP_003073;
CC DOMAIN: Two globular domains, G1 and G2, comprise the amino
CC terminus of the proteoglycan, while another globular region, G3,
CC makes up the COOH terminus. G1 contains link domains and thus
CC consists of three disulfide-bonded loop structures designated as
CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
CC and the chondroitin sulfate (CS) attachment domains lie between G2
CC and G3.
CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate

CC chains, N-linked and O-linked oligosaccharides.
CC -!- DISEASE: DEFECTS IN AGC1 ARE THE CAUSE OF NANOMELIA, A LETHAL
CC CONNECTIVE TISSUE DISORDER AFFECTING CARTILAGE DEVELOPMENT
CC (CHONDRODYSPLASIA) CHARACTERIZED BY SHORTENED AND MALFORMED LIMBS.
CC AGGREGAN IS TRUNCATED AT ITS C-TERMINAL IN THE CS-2 BINDING DOMAIN
CC AND IS NOT ANYMORE SECRETED FROM THE CHONDROCYTES.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
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CC -----
CC EMBL; L21913; AAB19128.1; -;
DR EMBL; M38187; AAA48731.1; -;
DR EMBL; M88101; -; NOT ANNOTATED_CDS.
DR EMBL; S74657; AAC60751.1; -;
DR EMBL; S74656; AAC60751.1; JOINED.
DR EMBL; J04028; AAA48719.1; -;
DR EMBL; M13993; AAA48720.1; -;
DR PIR; I50421; I50421.
DR HSSP; P08709; 1BF9.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR000152; Asx_hydroxyl_s.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR003324; SGXSG.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF02339; SGXSG; 56.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; Xlink; 4.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 4.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS01241; LINK; 4.
KW Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
KW Alternative splicing; Repeat; Immunoglobulin domain.
FT SIGNAL 1 16
FT CHAIN 17 2109 AGGREGAN CORE PROTEIN.
FT DOMAIN 34 143 IG-LIKE V-TYPE.
FT DOMAIN 166 243 LINK 1.
FT DOMAIN 264 346 LINK 2.
FT DOMAIN 537 614 LINK 3.
FT DOMAIN 635 716 LINK 4.
FT DOMAIN 1363 1742 19 X 20 AA TANDEM-REPEAT

FT	DOMAIN	1855	1892	EGF-LIKE.
FT	DOMAIN	1901	2019	C-TYPE LECTIN.
FT	DOMAIN	2023	2081	SUSHI.
FT	DOMAIN	48	137	G1-A.
FT	DOMAIN	148	243	G1-B.
FT	DOMAIN	249	346	G1-B'.
FT	DOMAIN	519	613	G2-B.
FT	DOMAIN	620	715	G2-B'.
FT	DOMAIN	718	803	KS.
FT	DOMAIN	805	1264	CS-1.
FT	DOMAIN	1265	1742	CS-2.
FT	DOMAIN	1893	2109	G3.
FT	DISULFID	51	129	BY SIMILARITY.
FT	DISULFID	171	242	BY SIMILARITY.
FT	DISULFID	195	216	BY SIMILARITY.
FT	DISULFID	269	345	BY SIMILARITY.
FT	DISULFID	293	314	BY SIMILARITY.
FT	DISULFID	542	613	BY SIMILARITY.
FT	DISULFID	566	587	BY SIMILARITY.
FT	DISULFID	640	715	BY SIMILARITY.
FT	DISULFID	664	685	BY SIMILARITY.
FT	DISULFID	1859	1870	BY SIMILARITY.
FT	DISULFID	1864	1879	BY SIMILARITY.
FT	DISULFID	1881	1890	BY SIMILARITY.
FT	DISULFID	1897	1908	BY SIMILARITY.
FT	DISULFID	1925	2017	BY SIMILARITY.
FT	DISULFID	1993	2009	BY SIMILARITY.
FT	DISULFID	2024	2067	BY SIMILARITY.
FT	DISULFID	2053	2080	BY SIMILARITY.
FT	CARBOHYD	76	76	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	122	122	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	330	330	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	388	388	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	439	439	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	644	644	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	700	700	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	765	765	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	801	801	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSP LIC	1856	1892	Missing (in isoform 2).
FT				/FTid=VSP 003073.
FT	CONFLICT	362	362	E -> D (IN REF. 3).

Query Match

Best Local Similarity

Matches

42; Conservative

28; Mismatches

58; Indels

40; Gaps

8;

QY	15	ORPCYKVIYFHDTSRRLNFEFAKEACRRDGGQLVSISEDEQKLIKFIENLLPSDGD	73
Db	1905	QGH CYR--HFEE---RETWMDAESRCREHQAHLSIITPEEQEFVNSHAQ-----DYQ	1952
QY	74	WIGLRRREKQSNSTACQDLYAWTDGSI SQFRNWNVDEPS----CGSEVCVVMYHQPSAP	129
Db	1953	WIGLSDR-----AVENDFRWSDGHS LQFENWRPNQPDNFFFFAGEDCVVM IWHQG--	2002
QY	130	AGIGGPYMFQWDDRCNMKNFICKYS-----DEKPAVPSREAEGETE	173
Db	2003	-----EWNDVPCNYHLPTCKKGTVACGDPVVENARTFGRK D	2041

Search completed: September 9, 2004, 22:54:11
Job time : 16.0369 secs

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17	169	15.3	217	11	Q8C4F8	Q8c4f8 mus musculu
18	165.5	15.0	742	11	Q8K4Q8	Q8k4q8 mus musculu
19	165.5	15.0	742	11	Q8C979	Q8c979 mus musculu
20	161.5	14.6	134	5	Q9XYX3	Q9xyx3 hydra magni
21	159.5	14.4	742	11	Q8VIF6	Q8vif6 mus musculu
22	158	14.3	142	11	Q8CJ86	Q8cj86 mus musculu
23	158	14.3	142	11	Q8BHK7	Q8bhk7 mus musculu
24	158	14.3	295	11	Q91ZW4	Q91zw4 mus musculu
25	158	14.3	311	11	Q9D8V4	Q9d8v4 mus musculu
26	158	14.3	325	11	Q91ZX0	Q91zx0 mus musculu
27	157	14.2	158	13	Q90WI7	Q90wi7 bungarus fa
28	156	14.1	323	11	Q8CJ91	Q8cj91 mus musculu
29	156	14.1	339	6	Q95244	Q95244 sus scrofa
30	155	14.0	293	11	Q8BGZ0	Q8bgz0 mus musculu
31	155	14.0	323	11	Q8CJ94	Q8cj94 mus musculu
32	155	14.0	323	11	Q8CJ93	Q8cj93 mus musculu
33	155	14.0	323	11	Q8CJ88	Q8cj88 mus musculu
34	155	14.0	379	11	Q7TMA7	Q7tma7 mus musculu
35	155	14.0	473	11	Q7TSP9	Q7tsp9 mus musculu
36	155	14.0	477	11	Q7TSQ7	Q7tsq7 mus musculu
37	155	14.0	504	11	Q7TSQ0	Q7tsq0 mus musculu
38	155	14.0	534	11	Q7TSQ1	Q7tsq1 mus musculu
39	155	14.0	1152	13	Q90WM2	Q90wm2 xenopus lae
40	154	13.9	322	11	Q8CJ89	Q8cj89 mus musculu
41	154	13.9	323	11	Q8CJ92	Q8cj92 mus musculu
42	153	13.8	446	4	Q7Z5K9	Q7z5k9 homo sapien
43	152.5	13.8	485	6	Q95LG3	Q95lg3 odocoileus
44	152	13.7	158	13	Q90WI6	Q90wi6 bungarus mu
45	151.5	13.7	652	4	Q8IXK1	Q8ixk1 homo sapien

ALIGNMENTS

RESULT 1
Q8TAY8
ID Q8TAY8 PRELIMINARY; PRT; 374 AA.
AC Q8TAY8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to unnamed protein product.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025407; AAH25407.1; -
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 374 AA; 42312 MW; FC214E6BC9E578D9 CRC64;

Query Match	100.0%;	Score 1106;	DB 4;	Length 374;
Best Local Similarity	100.0%;	Pred. No. 4.6e-98;		
Matches 204;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSI	DEQKLI	60
Db	24	GRLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSI	DEQKLI	83
QY	61	KFIENLLPSDGFHWIGLRRRREEKQSNSTACQDLYAWTDGSI	SQFRNWWYDEPSCGSEVCV	120
Db	84	KFIENLLPSDGFHWIGLRRRREEKQSNSTACQDLYAWTDGSI	SQFRNWWYDEPSCGSEVCV	143
QY	121	VMYHQPSAPAGIGGPGYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP		180

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: September 9, 2004, 22:47:24 ; Search time 72.1769 Seconds
(without alignments)
891.777 Million cell updates/sec

Title: US-09-887-855-2_COPY_24_227
Perfect score: 1106
Sequence: 1 GRLLSGQPVCRGGTQRPCYK.....BEDAKTTFKESREALNLAY 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1106	100.0	374	4	Q8TAY8	Q8tay8 homo sapien
2	1106	100.0	374	4	Q96NF3	Q96nf3 homo sapien
3	1102	99.6	374	4	Q96NC5	Q96nc5 homo sapien
4	945.5	85.5	374	11	Q9Z209	Q9z209 cricetus
5	803.5	72.6	211	11	Q8C351	Q8c351 mus musculu
6	580	52.4	246	11	Q8BMT7	Q8bmt7 mus musculu
7	580	52.4	292	11	Q8BVU2	Q8bvut mus musculu
8	513	46.4	236	4	Q7Z798	Q7z798 homo sapien
9	504.5	45.6	232	4	Q7Z799	Q7z799 homo sapien
10	500	45.2	236	4	Q7Z7A0	Q7z7a0 homo sapien
11	185	16.7	1290	13	Q9W6E1	Q9w6el gallus gall
12	178.5	16.1	1456	11	Q61830	Q61830 mus musculu
13	177.5	16.0	1348	5	Q25199	Q25199 hydra atten
14	176.5	16.0	1479	4	Q9Y5P9	Q9y5p9 homo sapien
15	176.5	16.0	1479	4	Q9UBG0	Q9ubg0 homo sapien
16	170.5	15.4	1479	11	Q64449	Q64449 mus musculu

Db 144 VMYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 203

QY 181 EETQEDAKTKFKESREAAALNLAY 204

Db 204 EETQEDAKTKFKESREAAALNLAY 227

RESULT 2

Q96NF3

ID Q96NF3 PRELIMINARY; PRT; 374 AA.

AC Q96NF3;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein FLJ30977.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,

RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,

RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,

RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,

RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,

RT "NEDO human cDNA sequencing project.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK055539; BAB70946.1; -.

DR GO; GO:0005529; F:sugar binding; IEA.

DR InterPro; IPR001304; LECTIN_C.

DR Pfam; PF00059; lectin_c; 1.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.

KW Hypothetical protein.

SQ SEQUENCE 374 AA; 42280 MW; 8AE64E6BC9E56DCD CRC64;

Query Match 100.0%; Score 1106; DB 4; Length 374;

Best Local Similarity 100.0%; Pred. No. 4.6e-98;

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLE 60

Db 24 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLE 83

QY 61 KFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWNVYDEPSCGSEVCV 120

Db 84 KFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWNVYDEPSCGSEVCV 143

QY 121 VMYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 180

Db 144 VMYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 203

QY 181 EETQEDAKTKFKESREAAALNLAY 204

Db 204 EETQEDAKTKFKESREAAALNLAY 227

RESULT 3

Q96NC5

ID Q96NC5 PRELIMINARY; PRT; 374 AA.

AC Q96NC5;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein FLJ31092.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,

RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,

RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,

RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,

RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,

RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,

RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,

RA Isogai T.,

RT "NEDO human cDNA sequencing project.";

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK055654; BAB70978.1; -.

DR GO; GO:0005529; F:sugar binding; IEA.

DR InterPro; IPR001304; LECTIN_C.

DR Pfam; PF00059; lectin_c; 1.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.

KW Hypothetical protein.

SQ SEQUENCE 374 AA; 42310 MW; CBF74E676E23BA16 CRC64;

Query Match 99.6%; Score 1102; DB 4; Length 374;

Best Local Similarity 99.5%; Pred. No. 1.1e-97;

Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLE 60

Db 24 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLE 83

QY 61 KFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWNVYDEPSCGSEVCV 120

Db 84 KFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWNVYDEPSCGSEVCV 143

QY 121 VMYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 180

Db 144 VMYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 203

QY 181 EETQEDAKTKFKESREAAALNLAY 204

Db 204 EETQEDAKTKFKESREAAALNLAY 227

RESULT 4

Q9Z209

ID Q9Z209 PRELIMINARY; PRT; 374 AA.

AC Q9Z209;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Layilin.

OS Cricetulus griseus (Chinese hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Cricetulus.

OX NCBI_TaxID=10029;

RN [1]

RP SEQUENCE FROM N.A.

RA Borowsky M.L., Hynes R.O.;

RT "Layilin, a novel talin-binding transmembrane protein homologous with

RT C-type lectins, is localized in membrane ruffles.";

RL J. Cell Biol. 143:0-0(1998).

DR EMBL; AF033673; AAC68695.1; -.

DR HSSP; P22897; 1EGG.

DR GO; GO:0005529; F:sugar binding; IEA.

DR InterPro; IPR001304; LECTIN_C.

DR Pfam; PF00059; lectin_c; 1.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.

SQ SEQUENCE 374 AA; 42435 MW; 298A8BA24FB04E1C CRC64;

Query Match 85.5%; Score 945.5; DB 11; Length 374;

Best Local Similarity 85.9%; Pred. No. 1.3e-82;

Matches 176; Conservative 9; Mismatches 19; Indels 1; Gaps 1;

```

Query Match      72.6%; Score 803.5; DB 11; Length 211;
Best Local Similarity 79.8%; Pred. No. 3e-69;
Matches 150; Conservative 9; Mismatches 20; Indels 9; Gaps 2;

QY   1 GRLLS-----GQPVCRGGTQRPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSIES 52
      |||||          |||||:|||||||:|||||||:|||||||:
Db   24 GRLLSASDLPRGGQLVCRGGTTRRPCYKVIYFHDAFQRLNFEAEKETCMEDGGQLVSJET 83

QY   53 EDEQKLIKFIEIENLLPSDGDFWIGLRRREEKQSNSTACODLYAWTDGSIQFRNWYYVDEP 112
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   84 EDEQRLIEKFIEIENLLASDGFWIGLKRLEEKQSNNTACODLYAWTDGSTSQFRNWYYVDEP 143

QY   113 SCGSEVCVMYHQPSAPAGIGGPYMFQWNDDRCNMKNPFICKYSDEKPA-VPSREAECEE 171
       |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   144 SCGSEVCVMYHQPSAPPGIGGSYMFQWNDDRCNMKNPFICKYHDDKPSTTPSIWPGGEA 203

QY   172 TELTTPVL 179
       |||||:
Db   204 TEPATPLL 211

RESULT 6
Q8BMI7
ID Q8BMI7 PRELIMINARY; PRT; 246 AA.
AC Q8BMI7;
```

DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	C-type lectin protein MT75 homolog.
GN	CHODL
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Forelimb;
RX	MEDLINE=22354683; PubMed=12466851;
RA	The FANTOM Consortium,
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs.";
RL	Nature 420:563-573(2002).
DR	EMBL; AK031063; BAC27234.1; -.
DR	MGD; MGI:2179069; Chodl.
DR	GO; GO:0005529; F:sugar binding; IEA.
DR	InterPro; IPR001304; Lectin_C.
DR	Pfam; PF00059; lectin_C; 1.
DR	SMART; SM00034; CLECT; 1.
DR	PROSITE; PS50041; C_TYPE_LLECTIN 2; 1.
SQ	SEQUENCE 246 AA; 27394 MW; E872660C58267752 CRC64;
Query Match 52.4%; Score 580; DB 11; Length 246;	
Best Local Similarity 57.9%; Pred. No. 1.1e-47;	
Matches 110; Conservative 26; Mismatches 40; Indels 14; Gaps 5;	
QY	2 RLLSGQPVCRGGTQRPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSI EDEQKLI EK 61
Db	23 RVVSGQKVCADVKHPCYKWAYFHELSSRVSFQEARLACESEGGVLLSLENAEQKLIES 82
QY	62 FIENLLP-----SDGDFWIGLRRREKQSNSTACQDLVYAWTDGSGISQFRNWWYVDEPSCGS 116
Db	83 MLQNLTKPGTGISDGDWIGLRLSGDGT-SGACPDLYQWSDGSSQFRNWWYVDEPSCGS 141
QY	117 EVCVVMYHGPSAPAGIGGYPYMFQWNDRCNMKNFNICKYSDE-KPAVPSRAEAGEETELT 175
Db	142 EKCVVMYHQPANTANGLGGPYLYQWNDRCNMKNYICKYEPIHPTPEA-----EKPYL 196
QY	176 TPVLPEETQE 185
Db	197 NQ--PEETHE 204
RESULT 7	
Q8BVU2	PRELIMINARY; PRT; 292 AA.
ID	Q8BVU2
AC	Q8BVU2;
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	C-type lectin protein MT75 homolog.
GN	CHODL
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Head;
RX	MEDLINE=22354683; PubMed=12466851;
RA	The FANTOM Consortium,
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs.";
RL	Nature 420:563-573(2002).
DR	EMBL; AK076523; BAC36378.1; -.
DR	MGD; MGI:2179069; Chodl.
DR	GO; GO:0005529; F:sugar binding; IEA.

RESULT 11
Q9W6E1 PRELIMINARY; PRT; 1290 AA.
AC Q9W6E1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Neurocan core protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309833; PubMed=10851024;
RA Li H., Leung T.C., Hoffman S., Balsamo J., Lilien J.;
RT "Coordinate Regulation of Cadherin and Integrin Function by the
RT Chondroitin Sulfate Proteoglycan Neurocan.";
RL J. Cell Biol. 149:1275-1288(2000).
DR EMBL; AF116856; AAD24546.2; -.
DR HSSP; P08709; 1BF9.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; Xlink; 2.
DR PRINTS; PRO0010; EGFBL00D.
DR PRINTS; PRO1265; LINKMODULE.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG_1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW EGF-like domain.
SQ SEQUENCE 1290 AA; 138877 MW; 182BD86D0E40BE78 CRC64;
Query Match 16.7%; Score 185; DB 13; Length 1290;
Best Local Similarity 34.7%; Pred. No. 8.6e-09;
Matches 50; Conservative 18; Mismatches 42; Indels 34; Gaps 8;
QY 15 QRPCYKVIYFHDTSRRNLNFEAEKACRRDGGQLVSISEDEQKLIKFIENLLPSDGDWF 74
DB 1064 QGHCVR--YF---SRRRSWEDAERDCRRRAGHLTSIHQSDEHGFINSF-----GHENTW 1112
QY 75 IGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS---CGSEVCVVMY-HQPSAPA 130
DB 1113 IGLNDRIVEQD-----FQWTDNTGLQYENWRNQDNFFAGGDCVVLVSHE----- 1159

QY 131 GIGGPYMFQWDDRCNMKNFNICK 154
DB 1160 -IG-----KWNDVPCNYNLPYICK 1177
RESULT 12
Q61830 PRELIMINARY; PRT; 1456 AA.
AC Q61830;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Macrophage mannose receptor precursor.
GN MRC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=93043353; PubMed=1421407;
RA Harris N., Rits M., Chang G., Ezekowitz R.B.;
RT "Characterization of the murine macrophage mannose receptor.";
RL Blood 80:2363-2373(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RA Super M.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBSJ databases.
DR EMBL; Z11974; CAA78028.1; -.
DR PIR; A48925; A48925.
DR PDB; 1DQG; 10-MAY-00.
DR PDB; 1DQO; 10-MAY-00.
DR PDB; 1FWU; 17-JAN-01.
DR PDB; 1FWV; 17-JAN-01.
DR MGD; MGI:97142; Mrcl.
DR GO; GO:0009928; C:cell surface (sensu Magnoliophyta); IDA.
DR GO; GO:0005537; F:mannose binding; IDA.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR008997; RicinB_like.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin_c; 8.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 6.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS50231; RICIN_B_LLECTIN; 1.
KW Receptor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1456 MACROPHAGE MANNOSE RECEPTOR.
SQ SEQUENCE 1456 AA; 165065 MW; 4EBD3F1B8619A594 CRC64;
Query Match 16.1%; Score 178.5; DB 11; Length 1456;
Best Local Similarity 25.9%; Pred. No. 4.2e-08;
Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;
QY 19 YKVIYFHDTSRRNLNFEAEKACRRDGGQLVSISEDEQKLIKFIENLLPSDGDWFGLR 78
DB 807 YKDYQYFSEKKEKTMNARRFCKKNFGDLATIKSESEKFLWKYI-NKNGGQSPYFIGML 865
QY 79 RREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY 136

Db 866 ISMDKK-----FIWMDGSKVDFVAWATGEPNFANDDENCVTMY-----TNSGF---- 908

QY 137 MFQWNDRCNMKNFICK---YSDEKPAVPSREAEGETELTTPVLPEETQE----- 185

Db 909 ---WINDINGYPNFCORHNSINATAMP-----TTPTTPGCKEGWHLYKNK 954

QY 186 -----EDAKKTFKESREAAALNL 202

Db 955 CFKIFGFANEKKSWQDARQACKGL 979

RESULT 13

Q25199

ID Q25199 PRELIMINARY; PRT; 1348 AA.

AC Q25199;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Tyrosine kinase receptor.

OS Hydra attenuata (Hydra) (Hydra vulgaris).

OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;

OC Hydridae; Hydra.

OX NCBI_TaxID=6087;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Irvine;

RX MEDLINE=20209407; PubMed=10744720;

RA Reidling J.C., Miller M.A., Steele R.E.;

RT "Sweet Tooth, a Novel Receptor Protein-tyrosine Kinase with C-type

RT Lectin-like Extracellular Domains.";

RL J. Biol. Chem. 275:10323-10330 (2000).

DR EMBL; L22612; AAA29218.2; -.

DR HSSP; P11362; 1FGK.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0005529; F:sugar binding; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR001304; Lectin_C.

DR InterPro; IPR003990; Pancreatins_ac.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR001245; Tyr_kinase.

DR InterPro; IPR008266; Tyr_kinase_AS.

DR Pfam; PF00059; lectin_c; 4.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR01504; PNCREATITSAP.

DR ProDom; PD000001; Prot_kinase; 2.

DR SMART; SM00034; CLECT; 4.

DR SMART; SM00219; TyrKC; 1.

DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 2.

DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 4.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.

SQ SEQUENCE 1348 AA; 156916 MW; 77D2122093227FEF CRC64;

Query Match 16.0%; Score 177.5; DB 5; Length 1348;

Best Local Similarity 28.0%; Pred. No. 4.8e-08;

Matches 47; Conservative 32; Mismatches 46; Indels 43; Gaps 8;

QY 4 LSGQPVC--RGGTQPC-----YKVIYFHDTSRRLNFEAEKACRRDGGQLVSIESEDE 55

Db 412 LSHRFICKVKRATNEYCAEGWTSYRIYCYFIYSIEFDWFKSFSSCONIGNLLSIENQEE 471

QY 56 QKLEKFIENLLPSDGD-FWIGLRR-----REKQSNSTACQDLYAWTDGSIQFRNWWY 108

Db 472 ---NRFIENDLIKNDKYGWIGLNKIWNLYLKNKR-----PEWSDNTYTQFFNWI 518

QY 109 VDEP--SCGSEVCVVMVHQPAPAGIGGYPWFQWDDRCNMKNFNICK 154

Db 519 TNQPDNNGIESCVEMVYN-----GWSDKCKVLNGFICK 553

RESULT 14

Q9Y5P9

ID Q9Y5P9 PRELIMINARY; PRT; 1479 AA.

AC Q9Y5P9;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Endocytic receptor Endo180.

GN ENDO180.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20148849; PubMed=10683150;

RA Sheikh H., Yarwood H., Ashworth A., Isacke C.;

RT "Endo180, an endocytic recycling glycoprotein related to the

RT macrophage mannose receptor is expressed on fibroblasts, endothelial

RT cells and macrophages and functions as a lectin receptor.";

RL J. Cell Sci. 113:1021-1032 (2000).

DR EMBL; AF134838; AAD30280.1; -.

DR HSSP; P02751; 2FN2.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0005529; F:sugar binding; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR000562; FN_Type_II.

DR InterPro; IPR001304; Lectin_C.

DR InterPro; IPR000566; Lipocln_cytFABP.

DR InterPro; IPR008997; RicinB_Like.

DR InterPro; IPR000772; Ricin_B_lectin.

DR Pfam; PF00040; fn2; 1.

DR Pfam; PF00059; lectin_c; 8.

DR PRINTS; PR00013; FNTYPEII.

DR ProDom; PD000995; FN_Type_II; 1.

DR SMART; SM00034; CLECT; 8.

DR SMART; SM00059; FN2; 1.

DR SMART; SM00458; RICIN; 1.

DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 3.

DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 8.

DR PROSITE; PS00023; FIBRONECTIN_2; 1.

DR PROSITE; PS00213; LIPOCALIN; 1.

DR PROSITE; PS50231; RICIN_B_LLECTIN; 1.

KW Receptor.

SQ SEQUENCE 1479 AA; 166669 MW; 9F4BAF355F036FCE CRC64;

Query Match 16.0%; Score 176.5; DB 4; Length 1479;

Best Local Similarity 30.4%; Pred. No. 6.7e-08;

Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;

QY 5 SGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSIESEDEQKLEKFI 64

Db 385 SWQPF-----QGHCVRL-----QAEKRSWQESKKACLRGGGDLVSIHMAELEFITKQIK 434

QY 65 NLLPSDGDWFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS---CGSEVCVV 121

Db 435 QEVE---ELWIGL-----NDLKLQMFNSDGLSVSFTHWHPFEPNFRDSDLDCVT 483

QY 122 MYHQPAPAGIGGYPWFQWDDRCNMKNFNICKYSDKPAVPSREAE 169

Db 484 IW---GPEG-----RWNDSPCNQSLPSICKKAGQLSQGAEEHDHG 520

RESULT 15

Q9UEG0

ID Q9UEG0 PRELIMINARY; PRT; 1479 AA.

AC Q9UEG0;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Urokinase receptor-associated protein UPAPAP.
GN KIAA0709.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Behrendt N., Jensen O.N., Engelholm L.H., Mortz E., Mann M., Dano K.;
RT "A urokinase receptor-associated protein with specific collagen-
RL binding properties.";
RN Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
DR EMBL; AF107292; AAF14192.1; -.
DR EMBL; AB014609; BAA31684.1; -.
DR HSSP; P02751; 2FN2.
DR Genew; HGNC:16875; MRC2.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR GO; GO:0005610; P:transport; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR008997; RicinB_like.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin_c; 8.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 3.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS50231; RICIN_B_LECTIN; 1.
KW Kinase; Receptor.
SQ SEQUENCE 1479 AA; 166654 MW; C7583EA78E2792D1 CRC64;

Query Match 16.0%; Score 176.5; DB 4; Length 1479;
Best Local Similarity 30.4%; Pred. No. 6.7e-08;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;

QY 5 SGQPVCRGGTQRPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI ESEDEQKLIK FIE 64
Db 385 SWQPF-----QGH CYRL-----QAEKRSWQESKKACLRGGGDLVSIHSM AELEFITKQIK 434

QY 65 NLLPSDGFWIGLRRRREEKQSNSTACQDLYAWTDGSI SQFRNMYVDEPS---CGSEVCVW 121
Db 435 QEVE---ELWIGL-----NDLKLQMNFEWSDGSLVSFTHWHPFPENNFRD SLEDCVT 483

QY 122 MYHQPSAPAGIGGYPYMFQWNDRCNMKNFICKYSDEKPAVPSREAE G 169
Db 484 IW----GPEG-----RWNDSPCNQSLPSICKKAGQLSQGA AEEDHG 520

RESULT 16
Q64449
ID Q64449 PRELIMINARY; PRT; 1479 AA.
AC Q64449;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lectin lambda.
GN MRC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96355501; PubMed=8702911;
RA Wu K., Yuan J., Lasky L.A.;
RT "Characterization of a novel member of the macrophage mannose receptor
RT type C lectin family.";
RL J. Biol. Chem. 271:21323-21330(1996).
DR EMBL; U56734; AAC52729.1; -.
DR PIR; T42710; T42710.
DR HSSP; P02751; 2FN2.
DR MGD; MGI:107818; Mrc2.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001128; Cytochrome P450.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR008997; RicinB_like.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin_c; 8.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00086; CYTOCHROME P450; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 3.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS50231; RICIN_B_LECTIN; 1.
SQ SEQUENCE 1479 AA; 167112 MW; 62D456E10B9B48C1 CRC64;

Query Match 15.4%; Score 170.5; DB 11; Length 1479;
Best Local Similarity 31.4%; Pred. No. 2.5e-07;
Matches 48; Conservative 22; Mismatches 48; Indels 35; Gaps 7;

QY 5 SGQPVCRGGTQRPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI ESEDEQKLIK FIE 64
Db 384 SWQPF-----QGH CYRL-----QAEKRSWQESKKACLRGGGDLVSIHSM AELEFITKQIK 433

QY 65 NLLPSDGFWIGLRRRREEKQSNSTACQDLYAWTDGSI SQFRNMYVDEPS---CGSEVCVW 121
Db 434 QEVE---ELWIGL-----NDLKLQMNFEWSDGSLVSFTHWHPFPENNFRD SLEDCVT 482

QY 122 MYHQPSAPAGIGGYPYMFQWNDRCNMKNFICK 154
Db 483 IW----GPEG-----RWNDSPCNQSLPSICK 504

RESULT 17
Q8C4F8
ID Q8C4F8 PRELIMINARY; PRT; 217 AA.
AC Q8C4F8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chondroitin sulfate proteoglycan 3 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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RESULT 20
Q9XXY3
ID Q9XXY3 PRELIMINARY; PRT; 134 AA.
AC Q9XXY3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Receptor protein-tyrosine kinase (Fragment).
GN HTK28.
OS Hydra magnipapillata (Hydra).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidea; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RX MEDLINE=20209407; PubMed=10744720;
RA Reidling J.C., Miller M.A., Steele R.E.;
RT "Sweet Tooth, a Novel Receptor Protein-tyrosine Kinase with C-type
RT Lectin-like Extracellular Domains.";
RL J. Biol. Chem. 275:10323-10330(2000).
DR EMBL; AF129528; AAD30040.1; -.
DR HSSP; P22897; LEGG.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Kinase; Tyrosine-protein kinase.
FT NON_TER 1
FT NON_TER 134
FT NON_TER 134
SQ SEQUENCE 134 AA; 15701 MW; E7B7211C881009BC CRC64;

Query Match 14.6%; Score 161.5; DB 5; Length 134;
Best Local Similarity 28.8%; Pred. No. 1e-07;
Matches 40; Conservative 23; Mismatches 51; Indels 25; Gaps 5;

QY 18 CYKVIYFHDTSRRLNFEFEAKEACRRDGGQLVSIIESEDEQKLIKFIENLLPSDGFWIGL 77
Db 16 CY--FFQNKTLQAKNWRDASLSQALGHLISIEDQAENFFILNFKDSSMQQDNYWIGL 73

QY 78 RRREEKQSNSTACQDLYAWTDGSGISQFRNWWYVDEPS--CGSEVVCVMYHQPSAPAGIGGP 135
Db 74 -----NDASNNREFRWSDDKIPQFFNWLPKKPNDQSEQNCV-----ETNSMG-- 116

QY 136 YMFQWDDRCNMKNFICK 154
Db 117 ----WNDENCDAINGFICK 131
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RESULT 21
Q8VIF6
ID Q8VIF6 PRELIMINARY; PRT; 742 AA.
AC Q8VIF6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Scavenger receptor with C-type lectin.
GN COLEC12 OR SRCL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21575692; PubMed=11718900;
RA Nakamura K., Funakoshi H., Tokunaga F., Nakamura T.;
RT "Molecular cloning of a mouse scavenger receptor with C-type lectin
RT (SRCL) (1), a novel member of the scavenger receptor family.";
RL Biochim. Biophys. Acta 1522:53-58(2001).
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DR EMBL; AB038519; BAB82497.1; -.
DR MGD; MGI:2152907; Colec12.
DR GO; GO:0006955; P:immune response; IDA.
DR GO; GO:0006910; P:phagocytosis, binding; IDA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor; LECTIN.
SQ SEQUENCE 742 AA; 81307 MW; 85A90D3AE881DB6B CRC64;

Query Match 14.4%; Score 159.5; DB 11; Length 742;
Best Local Similarity 33.1%; Pred. No. 1.3e-06;
Matches 49; Conservative 17; Mismatches 55; Indels 27; Gaps 8;

QY 18 CYKVIYFHDTSRRLNFEFEAKEACRRDGGQLVSIIESEDEQKLIKFIENLLPSDGFWIGL 77
Db 618 CY--YF--SLEKEILEDKLFCEKSSHLVFINSREEQWIKKH----TVGRESHWIGL 668

QY 78 RRREEKQSNSTACQDLYAWTDGSGISQFRNWWYVDEP--SCGSEVVCVMYHQPSAPAGIGGPY 136
Db 669 TDSEQESE-----WKWLDGSPVDYKNWKAGQPDNWGSG-----HGPGEDCA-GLIY 713

QY 137 MFWNDRCNMKNFICKYSDEKPAVPS 164
Db 714 AGQWDFQCDENNFICE--KEREAVPS 739

RESULT 22
Q8CJ86
ID Q8CJ86 PRELIMINARY; PRT; 142 AA.
AC Q8CJ86;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SIGNR1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Skin;
RX MEDLINE=22133304; PubMed=12137941;
RA Parent S.A., Zhang T., Chretien G., Clemas J.A., Figueroa D.J., Ky B.,
RA Blevins R.A., Austin C.P., Rosen H.;
RT "Molecular characterization of the murine SIGNR1 gene encoding a C-
RT type lectin homologous to human DC-SIGN and DC-SIGNR.";
RL Gene 293:33-46(2002).
DR EMBL; AF424802; AAN75597.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 142 AA; 16437 MW; 0CBB36A383D025EF CRC64;

Query Match 14.3%; Score 158; DB 11; Length 142;
Best Local Similarity 32.4%; Pred. No. 2.4e-07;
Matches 48; Conservative 21; Mismatches 45; Indels 34; Gaps 9;

QY 23 YFHDTSRRLNFEFEAKEACRRDGGQLVSIIESEDEQKLIKFIENLLPSDGFWIGLRRREE 82
Db 24 YFFSKSQ-RNWDNAVTAKEVKAQLVIINSDEEQ----TFLOQTSKAKGPTWGLSLDKK 78
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DR EMBL; AK007656; BAB25166.1; -
DR HSP; P22897; LEGG.
DR MGD; MGI:1916415; Cd209b.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 311 AA; 35618 MW; 92353503D2EF9041 CRC64;

Query Match 14.3%; Score 158; DB 11; Length 311;
Best Local Similarity 32.4%; Pred. No. 6.2e-07;
Matches 48; Conservative 21; Mismatches 45; Indels 34; Gaps 9;

QY 23 YFHDTSRRLNFEAEKACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD F WIGLRRREE 82
Db 193 YFPFSKSQR-NW NDAVTACKEVKAQLVIINSDEEQ----TFLQOTS KAKGPTW MGLSDLKK 247

QY 83 KQSNSTACQDLYAWTDGSI--SQFRN-WYVDEP-SCGSEVCVVMYHQPSAPAGIGGPYMF 138
Db 248 EAT-----WLWVDGSTLSSRFQKYWNRGEPNNIGEEDC VEF-----AGDG----- 287

QY 139 QWNDDRCNMKNFICKYSDEKPAVPSRE 166
Db 288 -WNDSKCELK KFWICK-----KSATPCTE 310
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Search completed: September 9, 2004, 22:56:41
Job time : 72.6769 secs

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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:39:44 ; Search time 85.2899 Seconds
(without alignments)
672.496 Million cell updates/sec

Title: US-09-887-855-2_COPY_25_227
Perfect score: 1100
Sequence: 1 RLLSGQPVCRGGTQPCYKV.....EEDAKTKFKESREALNLAY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1100	100.0	374	3	Aay93948 Amino aci
2	1100	100.0	374	4	Aae03651 Human ext
3	1100	100.0	374	5	Abb90203 Human pol
4	1100	100.0	374	5	Abg66680 Human nov
5	1100	100.0	374	6	Ada54522 Human pro
6	1100	100.0	387	4	Aam25796 Human pro
7	1096	99.6	374	6	Ada54574 Human pro
8	1090	99.1	374	3	Aay91490 Human sec
9	1086	98.7	382	2	Aay13367 Amino aci
10	1086	98.7	382	3	Adc78457 Human PRO
11	1086	98.7	382	4	Aab80235 Human PRO
12	1086	98.7	382	4	Aau29033 Human PRO
13	1086	98.7	382	6	Abu58409 Human PRO
14	1086	98.7	382	6	Abu71613 Human PRO
15	1086	98.7	382	6	Abu87957 Novel hum
16	1086	98.7	382	6	Abu84272 Human sec
17	1086	98.7	382	6	AbR66146 Human sec
18	1086	98.7	382	6	ABR65536 Human sec
19	1086	98.7	382	6	ABU99476 Human sec
20	1086	98.7	382	6	ABU82715 Human PRO
21	1086	98.7	382	6	ABU89836 Novel hum
22	1086	98.7	382	6	ABU71468 Human PRO
23	1086	98.7	382	6	ABR68085 Human sec
24	1086	98.7	382	6	ABU96138 Novel hum
25	1086	98.7	382	6	ABU92569 Human sec

26	1086	98.7	382	6	ABO08646 Human sec
27	1086	98.7	382	6	ABO02698 Human sec
28	1086	98.7	382	6	ABR74852 Human sec
29	1086	98.7	382	6	ABR94614 Human sec
30	1086	98.7	382	6	ABU85587 Human PRO
31	1086	98.7	382	6	ABU98747 Novel hum
32	1086	98.7	382	6	ABU97962 Novel hum
33	1086	98.7	382	6	ABU91668 Novel hum
34	1086	98.7	382	6	ABU71914 Human sec
35	1086	98.7	382	6	ABU89361 Human PRO
36	1086	98.7	382	6	ABU86202 Human sec
37	1086	98.7	382	6	ABU67415 Human sec
38	1086	98.7	382	6	ABU80443 Human PRO
39	1086	98.7	382	6	ABO01797 Novel hum
40	1086	98.7	382	6	ABR99361 Human sec
41	1086	98.7	382	6	ABR98751 Human sec
42	1086	98.7	382	6	ABO16274 Human sec
43	1086	98.7	382	6	ABR92174 Human sec
44	1086	98.7	382	6	ABO18815 Human sec
45	1086	98.7	382	6	ABR78236 Human sec

ALIGNMENTS

RESULT 1
AAY93948
ID AAY93948 standard; protein; 374 AA.
XX
AC AAY93948;
XX
DT 03-OCT-2000 (first entry)
XX
DE Amino acid sequence of a lectin ss3939 polypeptide.
XX
KW Human; lectin ss3939; chromosome 11; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21 /note= "signal peptide"
FT Domain 22..227 /note= "extracellular coding region"
FT Domain 228..248 /note= "predicted transmembrane domain"
FT Domain 249..374 /note= "predicted cytoplasmic or intracellular domain"
XX
PN WO200039296-A1.
XX
PD 06-JUL-2000.
XX
PF 22-DEC-1999; 99WO-US030523.
XX
PR 23-DEC-1998; 98US-0113820P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Anderson DA;
XX
DR WPI; 2000-452394/39.
XX
DR N-PSDB; AAA57382.
PT ss3939 nucleic acids, polypeptides and antibodies, useful for identifying
XX human chromosome 11 and diseases associated with it.
PS Claim 12; Page 8; 73pp; English.
XX
CC The present sequence represents a human lectin ss3939 polypeptide. The
polynucleotide sequence is a source of probes, which may be used to
identify nucleic acids encoding ss3939 proteins, to identify human
chromosome number 11, to map genes on human chromosome number 11, to

CC identify diseases associated with chromosome 11, as single-stranded sense
CC or antisense oligonucleotides to inhibit expression of polypeptides
CC encoded by the ss3939 gene, and for gene therapy. The ss3939 polypeptides
CC may be useful for developing treatments for diseases (none specified)
CC associated with defective or insufficient amounts of the polypeptides.
CC The antibodies may be useful for detecting the presence of ss3939
CC polypeptides
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 1100; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.3e-103;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRCGGTQPCYKVIYFHDTSRRLLNPFEEAKEACRRDGGQLVSIIESEDEQKLIK 60
Db |||||
QY 25 RLLSGQPVCRCGGTQPCYKVIYFHDTSRRLLNPFEEAKEACRRDGGQLVSIIESEDEQKLIK 84
Db |||||
QY 61 FIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIISQFRNRYVDEPSCGSEVCVV 120
Db |||||
QY 85 FIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIISQFRNRYVDEPSCGSEVCVV 144
QY 121 MYHQSAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db |||||
QY 145 MYHQSAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204
QY 181 ETQEEDAKKTFKESREAAALNLAY 203
Db |||||
QY 205 ETQEEDAKKTFKESREAAALNLAY 227

RESULT 2

AAE03651
ID AAE03651 standard; protein; 374 AA.
XX
AC AAE03651;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human extracellular matrix and cell adhesion molecule-15 (XMAD-15).
XX
KW Human; extracellular matrix and cell adhesion molecule; XMAD;
KW gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia;
KW Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy;
KW sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;
KW inflammatory disorder; acquired immune deficiency syndrome; AIDS;
KW Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma;
KW Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer;
KW glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis;
KW osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis;
KW infection; cell proliferative disorder; actinic keratosis; myeloma;
KW arteriosclerosis; neutrotropic; anticonvulsant; antithyroid; nephrotropic;
KW neuroprotective; dermatological.

Homo sapiens.

Key Location/Qualifiers
Peptide 1..24
Protein /label= Signal_peptide
25..374
Domain /note= "Mature human extracellular matrix and cell
adhesion molecule (XMAD)"
46..63
Domain /note= "C-type lectin domain"
163..176
Domain /note= "C-type lectin domain"
224..247
Domain /note= "Transmembrane motif"
328..348
Domain /note= "Transmembrane motif"

WO200142285-A2.

PD 14-JUN-2001.
XX
PF 05-DEC-2000; 2000WO-US032990.
XX
PR 10-DEC-1999; 99US-0172852P.
PR 16-DEC-1999; 99US-0172354P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Tang YT, Lal P, Burford N, Azimzai Y, Patterson C;
PI Baughn MR, Lu DAM, Shah P, Au-Young J;
XX
DR WPI; 2001-381632/40.
DR N-PSDB; AAD08059.
XX
PT New human extracellular matrix and cell adhesion molecules and
PT polynucleotide sequences encoding them, useful for diagnosis, prevention,
PT treatment of genetic, autoimmune and cell proliferative disorders.
XX
PS Claim 1; Page 108-109; 135pp; English.
XX

CC The present sequence is a human extracellular matrix and cell adhesion
CC molecule (XMAD). The XMAD is used for screening a compound for
CC effectiveness as an agonist or antagonist of XMAD. The identified agonist
CC or antagonist are used for treating a disease or condition associated
CC with decreased or increased expression of functional XMAD. The
CC polynucleotides encoding XMAD are useful in somatic or germline gene
CC therapy to correct a genetic deficiency, to express a conditionally
CC lethal gene product and to express a protein which affords protection
CC against intracellular parasites and also for diagnosis of disorders
CC associated with expression of XMAD. They are also used for generating
CC hybridisation probes useful in mapping the naturally occurring genomic
CC sequences and to create knock in humanised animals (pigs) or transgenic
CC animals (mice or rats) to model human diseases. Oligonucleotide or longer
CC fragments derived from the polynucleotide sequences may be used as
CC elements on a microarray. Antibodies which specifically bind XMAD may be
CC used for the diagnosis of disorders associated with the expression of
CC XMAD, or in assays to monitor patients being treated with XMAD. Diseases
CC diagnosed, prevented or treated include genetic disorders such as
CC adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's
CC disease, myotonic dystrophy, sickle cell anaemia, thalassaemia,
CC autoimmune/inflammatory disorders such as acquired immune deficiency
CC syndrome (AIDS), Addison's disease, allergies, anaemia, asthma,
CC atherosclerosis, Crohn's disease, diabetes mellitus, atopic dermatitis,
CC glomerulonephritis, multiple sclerosis, Grave's disease, osteoarthritis,
CC osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis,
CC bacterial, fungal, parasitic, protozoal and helminthic infections and
CC cell proliferative disorders, such as actinic keratosis, arteriosclerosis
CC and cancer including breast, bladder, bone marrow, brain and uterus
CC cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma

SQ Sequence 374 AA;

Query Match 100.0%; Score 1100; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.3e-103;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRCGGTQPCYKVIYFHDTSRRLLNPFEEAKEACRRDGGQLVSIIESEDEQKLIK 60
Db |||||
QY 25 RLLSGQPVCRCGGTQPCYKVIYFHDTSRRLLNPFEEAKEACRRDGGQLVSIIESEDEQKLIK 84
Db |||||
QY 61 FIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIISQFRNRYVDEPSCGSEVCVV 120
Db |||||
QY 85 FIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIISQFRNRYVDEPSCGSEVCVV 144
QY 121 MYHQSAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db |||||
QY 145 MYHQSAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204
QY 181 ETQEEDAKKTFKESREAAALNLAY 203
Db |||||
QY 205 ETQEEDAKKTFKESREAAALNLAY 227

QY 121 MYHPSAPAGIGGYPYMFQWDDRCNMKNFICKYSDKPAVPSRAEAGEETELTPVLPE 180
Db 145 MYHPSAPAGIGGYPYMFQWDDRCNMKNFICKYSDKPAVPSRAEAGEETELTPVLPE 204
QY 181 ETQEDAKTKTFKESREAAALNLAY 203
Db 205 ETQEDAKTKTFKESREAAALNLAY 227

RESULT 4
ABG66680
ID ABG66680 standard; protein; 374 AA.
XX
AC ABG66680;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human novel polypeptide #15.
XX
KW Human; inflammatory condition; shock; sepsis; immune response; cancer;
KW wound healing; central nervous system disease; haematopoiesis;
KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
KW bone degenerative disorder; periodontal disease; reperfusion injury;
KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
KW allergic condition; thrombolysis; thrombosis; coagulation disorder;
XX
OS Homo sapiens.
XX
PN WO200244340-A2.
XX
PD 06-JUN-2002.
XX
XX 30-NOV-2001; 2001WO-US047004.
PF
XX
PR 30-NOV-2000; 2000US-00728952.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;
PI Yamazaki V, Ujwal ML, Drmanac RT;
XX
DR WPI; 2002-508509/54.
DR N-PSDB; ABK94904.
XX
XX Novel nucleic acids and polypeptides for diagnosis, treatment of
PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
disorders, cancer and promoting wound healing.
Claim 10; Page 579-580; 672pp; English.
The invention relates to human novel polynucleotides and associated
polypeptides. The polynucleotides and polypeptides are useful for
treating inflammatory conditions such as arthritis, nephritis, Crohn's
disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
and cancer and for promoting wound healing. The sequences are used to
induce the proliferation of neural cells and regeneration of nerve and
brain tissue, and are useful for the treatment of central and peripheral
nervous system diseases and neuropathies, such as Alzheimer's disease,
Parkinson's disease, Huntington's disease and amyotrophic lateral
sclerosis. The sequences are involved in chemotactic or chemokinetic
activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
cell disorders and platelet disorders such as thrombocytopenia,
regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
growth, tissue repair, healing of burns, incisions, ulcers, treatment of
osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
disease. The sequences of the invention are also useful for gut
protection or regeneration and treatment of lung or liver fibrosis,
reperfusion injury in various tissues, immune deficiencies and disorders
including severe combined immunodeficiency (SCID), bacterial or fungal
infections, autoimmune disorders e.g. multiple sclerosis and myasthenia

RESULT 3
ABB90203
ID ABB90203 standard; protein; 374 AA.
XX
AC ABB90203;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2579.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US016450.
XX
PR 19-MAY-2000; 2000US-0205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
XX WPI; 2002-122018/16.
DR N-PSDB; ABL90612.
XX
XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.
XX
PS Claim 11; SEQ ID NO 2579; 2081pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 374 AA;
Query Match 100.0%; Score 1100; DB 5; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.3e-103;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI EDEQKLIK 60
Db 25 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI EDEQKLIK 84
QY 61 FIENLLPSDGDWFWIGLRRREEKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGSEVCW 120
Db 85 FIENLLPSDGDWFWIGLRRREEKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGSEVCW 144

CC gravis, allergic conditions such as asthma, thrombolysis or thrombosis
CC and coagulation disorders. Sequences ABG6666-ABG66758 represent human
CC novel polypeptides of the invention

XX SQ Sequence 374 AA;
Query Match 100.0%; Score 1100; DB 5; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.3e-103;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSISEDEQKLIK 60
Db 25 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSISEDEQKLIK 84
QY 61 FIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
Db 85 FIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 144
QY 121 MYHQSAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETELTTPVLPE 180
Db 145 MYHQSAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETELTTPVLPE 204
QY 181 ETQEDAKKTFKESREAAALNLAY 203
Db 205 ETQEDAKKTFKESREAAALNLAY 227

RESULT 5
ADA54522
ID ADA54522 standard; protein; 374 AA.
XX AC ADA54522;
XX DT 20-NOV-2003 (first entry)
XX DE Human protein, SEQ ID 2090.
XX KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX OS Homo sapiens.
XX PN EP1293569-A2.
XX PD 19-MAR-2003.
XX PF 21-MAR-2002; 2002EP-00006586.
XX PR 14-SEP-2001; 2001JP-00328381.
XX PR 24-JAN-2002; 2002US-0350435P.
XX PA (HELI-) HELIX RES INST.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-395539/38.
XX DR N-PSDB; ADA52883.
XX PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX PS Claim 14; SEQ ID NO 2090; 205pp; English.

CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins.

XX SQ Sequence 374 AA;
Query Match 100.0%; Score 1100; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.3e-103;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSISEDEQKLIK 60
Db 25 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSISEDEQKLIK 84
QY 61 FIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
Db 85 FIENLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 144
QY 121 MYHQSAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETELTTPVLPE 180
Db 145 MYHQSAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETELTTPVLPE 204
QY 181 ETQEDAKKTFKESREAAALNLAY 203
Db 205 ETQEDAKKTFKESREAAALNLAY 227

RESULT 6
AAM25796
ID AAM25796 standard; protein; 387 AA.
XX AC AAM25796;
XX DT 16-OCT-2001 (first entry)
XX DE Human protein sequence SEQ ID NO:1311.
XX KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiaggregant; haemostatic; vulnery; antiulcer; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder.

XX OS Homo sapiens.
XX PN WO200153455-A2.
XX PD 26-JUL-2001.
XX PF 22-DEC-2000; 2000WO-US035017.
XX PR 23-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-00488725.
XX PR 25-APR-2000; 2000US-00552317.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-457603/49.
XX DR N-PSDB; AAH99737.

XX PT Isolated human polynucleotides encoding polypeptides, useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection.

XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and cells
CC they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
CC antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders
XX
SQ Sequence 387 AA;

Query Match 100.0%; Score 1100; DB 4; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.4e-103;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIK 60
Db 38 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIK 97

QY 61 FIENLLPSDGDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWIYVDEPSCGSEVCVV 120
Db 98 FIENLLPSDGDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWIYVDEPSCGSEVCVV 157

QY 121 MYHOPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 158 MYHOPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 217

QY 181 ETQEDAKTKTFKESREAAALNLAY 203
Db 218 ETQEDAKTKTFKESREAAALNLAY 240

RESULT 7
ADA54574
ID ADA54574 standard; protein; 374 AA.
XX
AC ADA54574;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human protein, SEQ ID 2142.
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX
OS Homo sapiens.
XX
PN EP1293569-A2.
XX
PD 19-MAR-2003.
XX
PF 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
PR 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-395539/38.
DR N-PSDB; ADA52935.
XX
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 14; SEQ ID NO 2142; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 374 AA;

Query Match 99.6%; Score 1096; DB 6; Length 374;
Best Local Similarity 99.5%; Pred. No. 3.4e-103;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIK 60
Db 25 RLLSGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESEDEQKLIK 84

QY 61 FIENLLPSDGDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWIYVDEPSCGSEVCVV 120
Db 85 FIENLLPSDGDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWIYVDEPSCGSEVCVV 144

QY 121 MYHOPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHOPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204

QY 181 ETQEDAKTKTFKESREAAALNLAY 203
Db 205 ETQEDAKTKTFKESREAAALNLAY 227

RESULT 8
AAY91490
ID AAY91490 standard; protein; 374 AA.
XX
AC AAY91490;
XX
DT 29-JUN-2000 (first entry)
XX
DE Human secreted protein sequence encoded by gene 40 SEQ ID NO:163.
XX
KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;
KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
KW immune disease; inflammation; blood disorder; tumour.
XX
OS Homo sapiens.
XX
PN WO200006698-A1.
XX
PD 10-FEB-2000.
XX
PF 29-JUL-1999; 99WO-US017130.
XX
PR 30-JUL-1998; 98US-0094657P.
PR 05-AUG-1998; 98US-0095486P.
PR 06-AUG-1998; 98US-0095454P.
PR 06-AUG-1998; 98US-0095455P.
PR 12-AUG-1998; 98US-0096319P.
XX

PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;	
PI	Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;	
PI	Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;	
XX		
DR	WPI; 2000-195282/17.	
DR	N-PSDB; AAA26385.	
XX		
PT	New isolated human genes and the secreted polypeptides they encode,	
PT	useful for diagnosis and treatment of e.g. cancers, neurological	
PT	disorders, immune diseases, inflammation or blood disorders.	
XX		
PS	Claim 11; Page 483-484; 634pp; English.	
XX		
CC	The polynucleotide sequences given in AAA26346 to AAA26458 encode the	
CC	human secreted proteins given in AAY91451 to AAY91691. The human secreted	
CC	proteins can have activities based on the tissues and cells they are	
CC	expressed in. Examples of the activities are: cytostatic;	
CC	immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective;	
CC	antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;	
CC	asthma; antipsoriatic; and cardiac. The polynucleotides and their	
CC	corresponding secreted proteins are useful for preventing, treating or	
CC	ameliorating medical conditions, e.g. by protein or gene therapy. Also	
CC	pathological conditions can be diagnosed by determining the amount of the	
CC	proteins in a sample or by determining the presence of mutations in the	
CC	polynucleotides. Specific uses are described for each of the	
CC	polynucleotides, based on which tissues they are most highly expressed	
CC	in, and include developing products for the diagnosis or treatment of	
CC	cancer, tumours, neurodegenerative disorders, developmental abnormalities	
CC	and foetal deficiencies, blood disorders, diseases of the immune system,	
CC	autoimmune diseases, hepatic and renal disease, inflammation, allergies,	
CC	Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,	
CC	arthritis, infections, AIDS, spinal cord injuries, transplant rejection,	
CC	diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,	
CC	reproductive disorders, gastrointestinal disorders, respiratory disorders	
CC	and metabolic disorders. The proteins or polynucleotides can also be used	
CC	as food additives or preservatives. The proteins are also useful for	
CC	identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are	
XX	sequences used in the exemplification of the present invention	
SQ	Sequence 374 AA;	
Query Match 99.1%; Score 1090; DB 3; Length 374;		
Best Local Similarity 99.0%; Pred. NO. 1.4e-102;		
Matches 201; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSI ESEDEQKLIEX 60	
Db		
Db	25 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSI ESEDEQKLIEX 84	
QY	61 FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSI SQFRNYYVDEPSCGSEVCVV 120	
Db		
Db	85 FIENLLPSDGFWIGLRRREEKQSNSTXCDLYAWTDGSI SQFRNYYVDEPSCGSEVCVV 144	
QY	121 MYHQPSAPAGIGGPMYFQWDDRCNMKNFKICKYSDEKPAVPSREAEGETELTTPVLPE 180	
Db		
Db	145 MYHQPSAPAGIGGPMYFQWDDRCNMKNFKICKYSDEKPAVPSREAEGETELTTPVLPE 204	
QY	181 ETQEEDAKKTFKESREAAINLAY 203	
Db		
Db	205 ETQEEDAKKTFKESREAAINLAY 227	
RESULT 9		
AAY13367		
XX	ID AAY13367 standard; protein; 382 AA.	
AC	AAY13367;	
XX		
DT	25-JUN-1999 (first entry)	
XX		

XX	Secreted protein; transmembrane protein; human; enterocolitis;	
KW	Zollinger-Ellison syndrome; gastrointestinal ulceration;	
KW	congenital microvillus atrophy; skin disease; cell growth;	
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;	
KW	Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;	
KW	dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;	
KW	wound healing; tissue repair.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9914328-A2.	
XX		
PD	25-MAR-1999.	
XX		
PF	16-SEP-1998; 98WO-US019330.	
XX		
PR	17-SEP-1997; 97US-0059113P.	
PR	17-SEP-1997; 97US-0059115P.	
PR	17-SEP-1997; 97US-0059117P.	
PR	17-SEP-1997; 97US-0059119P.	
PR	17-SEP-1997; 97US-0059121P.	
PR	17-SEP-1997; 97US-0059122P.	
PR	17-SEP-1997; 97US-0059184P.	
PR	18-SEP-1997; 97US-0059263P.	
PR	18-SEP-1997; 97US-0059266P.	
PR	15-OCT-1997; 97US-0062125P.	
PR	17-OCT-1997; 97US-0062285P.	
PR	17-OCT-1997; 97US-0062287P.	
PR	21-OCT-1997; 97US-0063486P.	
PR	24-OCT-1997; 97US-0062814P.	
PR	24-OCT-1997; 97US-0062816P.	
PR	24-OCT-1997; 97US-0063045P.	
PR	24-OCT-1997; 97US-0063120P.	
PR	24-OCT-1997; 97US-0063121P.	
PR	24-OCT-1997; 97US-0063127P.	
PR	24-OCT-1997; 97US-0063128P.	
PR	27-OCT-1997; 97US-0063327P.	
PR	27-OCT-1997; 97US-0063329P.	
PR	28-OCT-1997; 97US-0063541P.	
PR	28-OCT-1997; 97US-0063542P.	
PR	28-OCT-1997; 97US-0063544P.	
PR	28-OCT-1997; 97US-0063549P.	
PR	28-OCT-1997; 97US-0063550P.	
PR	28-OCT-1997; 97US-0063564P.	
PR	29-OCT-1997; 97US-0063435P.	
PR	29-OCT-1997; 97US-0063704P.	
PR	29-OCT-1997; 97US-0063732P.	
PR	29-OCT-1997; 97US-0063734P.	
PR	29-OCT-1997; 97US-0063735P.	
PR	29-OCT-1997; 97US-0063738P.	
PR	29-OCT-1997; 97US-0064215P.	
PR	31-OCT-1997; 97US-0063870P.	
PR	31-OCT-1997; 97US-0064103P.	
PR	03-NOV-1997; 97US-0064248P.	
PR	07-NOV-1997; 97US-0064809P.	
PR	12-NOV-1997; 97US-0065186P.	
PR	17-NOV-1997; 97US-0065846P.	
PR	18-NOV-1997; 97US-0065693P.	
PR	21-NOV-1997; 97US-0066120P.	
PR	21-NOV-1997; 97US-0066364P.	
PR	24-NOV-1997; 97US-0066453P.	
PR	24-NOV-1997; 97US-0066466P.	
PR	24-NOV-1997; 97US-0066511P.	
PR	24-NOV-1997; 97US-0066770P.	
PR	24-NOV-1997; 97US-0066772P.	
PR	25-NOV-1997; 97US-0066840P.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;	
XX		

DR	N-PSDB; AAX52238.
XX	New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration.
PT	
XX	Claim 12; Fig 50; 320pp; English.
PS	
XX	AAV13344-403 represent secreted and transmembrane human proteins. The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract
XX	
SQ	Sequence 382 AA;
	Query Match 98.7%; Score 1086; DB 2; Length 382;
	Best Local Similarity 96.2%; Pred. No. 3.7e-102;
	Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY	1 RLLS-----GQVCRGGTQRPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSIESE 52
Db	25 RLLSASDLRLGGQPVRGGTQRPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSIESE 84
QY	53 DEQKLIEFIENLLPSDGFWIGLRRREKQSNSTACODLYAWTDGSISQFRNWWYDEPS 112
Db	85 DEQKLIEFIENLLPSDGFWIGLRRREKQSNSTACODLYAWTDGSISQFRNWWYDEPS 144
QY	113 CGSEVCVMYHQSPAPAGIGPYMFQWNDDRCNMKNPFICKYSDEKPAVPSSRAEGETE 172
Db	145 CGSEVCVMYHQSPAPAGIGPYMFQWNDDRCNMKNPFICKYSDEKPAVPSSRAEGETE 204
QY	173 LTPVLPEETQEEDAKTFKESREAALNLAY 203
Db	205 LTPVLPEETQEEDAKTFKESREAALNLAY 235
RESULT 10	
ADC78457	
ID	ADC78457 standard; protein; 382 AA.
XX	ADC78457;
XX	
DT	01-JAN-2004 (first entry)
XX	
DE	Human PRO234 protein.
XX	
KW	antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
KW	neotropic; neuroprotective; vasotropic; chemotactic; angiogenic;
KW	neutrophic; osteopathic; antiasthmatic; antifarthritic; antirheumatic;
KW	antiartherosclerotic; cardiant; antidiabetic; cerebroprotective;
KW	thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
KW	gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
KW	Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
KW	nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
KW	asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
KW	atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
KW	diabetes; stroke; gene therapy; transgenic; PRO; human.
XX	

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OS Homo sapiens.
XX WO200015796-A2.
XX PN
XX 23-MAR-2000.
XX PD
XX PF 15-SEP-1999; 99WO-US021090.
XX PR 16-SEP-1998; 98WO-US019330.
XX PP
XX (GETH ) GENENTECH INC.
XX PA
XX PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
XX PI Yuan J;
XX PP
XX WPI; 2000-271434/23.
XX DR N-PSDB; ADC78456.
XX PR
XX Novel nucleic acids encoding secreted and transmembrane polypeptides with
XX PT homology, e.g. to growth and cancer-associated antigens.
XX PS Claim 12; SEQ ID NO 137; 355pp; English.
XX PP
XX The invention relates to a novel nucleic acid encoding a PRO polypeptide.
XX CC The polypeptides and polynucleotides of the invention may be useful as
XX CC research tools and as therapeutics for treating enterocolitis, Zollinger-
XX CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
XX CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
XX CC scarring and wound healing, nerve repair, thrombosis, bone and/or
XX CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
XX CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
XX CC infertility, premature aging, AIDS, diabetes complications and stroke.
XX CC The molecules may also be utilised during gene therapy procedures and
XX CC transgenic animal production. The current sequence is that of the human
XX CC PRO protein of the invention.
XX PP
XX Sequence 382 AA;
XX
Query Match 98.7%; Score 1086; DB 3; Length 382;
Best Local Similarity 96.2%; Pred.No. 3.7e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE 52
Db 25 RLLSASDLRLRGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESE 84

QY 53 DEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLAYWTDGSIQFRNWWYVDEPS 112
Db 85 DEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLAYWTDGSIQFRNWWYVDEPS 144

QY 113 CGSEVCVMYHQPSAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETE 172
Db 145 CGSEVCVMYHQPSAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETE 204

QY 173 LITPVLPEETQEEDAKKTFKESREAAINLAY 203
Db 205 LITPVLPEETQEEDAKKTFKESREAAINLAY 235

RESULT 11
AAB80235
ID AAB80235 standard; protein; 382 AA.
XX AAB80235;
XX AC
XX 24-APR-2001 (first entry)
XX DE
XX Human PRO234 protein.
XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;

```

ophthalmological; gene therapy; skin disease; gastrointestinal disorder; ischaemia; inflammation.

Homo sapiens.

WO200104311-A1.

18-JAN-2007

22-FEB-2000: 2000WO-US004414.

07-III.-1999: 99IS-0143048P.

07-UUT-1999; 99US-0145698P.
26-UUT-1999; 99US-0145698P.

28-JUL-1999: 99US-0146222P:

08-SEP-1999; 99WO-US020594.

13-SEP-1999; 99WO-US020944.

15-SEP-1999; 99WO-US021090.

15-SEP-1999; 99WO-US021547.

05-OCT-1999; 99WO-US023089.

29-NOV-1999; 99WO-US028214.

30-NOV-1999; 99WO-US028313.

02-DEC-1999; 99WO-US028564.

02-DEC-1999; 99WO-US028565.
10 DEC 1999; 99WO-US028565.

T6-DEC-1999;
00 DEC 1999
08 DEC 1999
16 DEC 1999;
23 DEC 1999

Z0=DEC-1999;
Z0=DEC-1999;
99WC-USU3030TII.
99WC-USU3030TII.
99WC-USU3030TII.

20-DEC-1993; 59MC-US030333
05-TAN-2000: 200WC-US000219

ET2000050-CM0007 ; 00007-NYN-EN

(GETH) GENENTECH INC.

Ashkenazi AJ. Botstein D. Desnovers L. Eaton DL. Ferrara N;

Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;

Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

Williams PM, Wood WI;

WPI; 2001-081051/

N-PSDB; AAF72396.

Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease).

Claim 1: Fig 50: 393pp: English.

The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.

Sequence 382 AA;

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Query Match          98.7%; Score 1086; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.7e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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OV 1 RLLS-----GOPVCRGGTORPCYKVIYFHDTSRRLNFEAAKEACRRDGGQLVSIIE 52

25 RLI-SASDPLIRGGOPVCRGGTORPCYKVIYFHDTSRRLNFEAAKEACRRDGGOLVSE 84

CV 53 DEOKLIEKFIENLLPSDGDWIGLRREEKOSNSTACODLYAWTDGSI SOFRNWYVDEPS 112

85 DECKTEKFIENLLPSDGDWEIGLBRREEKOSNSTACODLYAWTDGSI SOFRNWVDEPS 144

PF	21-JUN-2002;	2002US-00176492;	
XX			
PR	18-SEP-1997;	97US-0059263P.	
PR	18-SEP-1997;	97US-0059266P.	
PR	17-OCT-1997;	97US-0062250P.	
PR	21-OCT-1997;	97US-0063486P.	
PR	24-OCT-1997;	97US-0063120P.	
PR	24-OCT-1997;	97US-0063121P.	
PR	28-OCT-1997;	97US-0063540P.	
PR	28-OCT-1997;	97US-0063541P.	
PR	28-OCT-1997;	97US-0063544P.	
PR	28-OCT-1997;	97US-0063564P.	
PR	29-OCT-1997;	97US-0063734P.	
PR	31-OCT-1997;	97US-0063870P.	
PR	31-OCT-1997;	97US-0064103P.	
PR	13-NOV-1997;	97US-0065311P.	
PR	21-NOV-1997;	97US-0066120P.	
PR	24-NOV-1997;	97US-0066466P.	
PR	24-NOV-1997;	97US-0066772P.	
PR	11-DEC-1997;	97US-0069335P.	
PR	12-DEC-1997;	97US-0069425P.	
PR	17-DEC-1997;	97US-0069870P.	
PR	18-DEC-1997;	97US-0068017P.	
PR	10-MAR-1998;	98US-0077450P.	
PR	11-MAR-1998;	98US-0077632P.	
PR	11-MAR-1998;	98US-0077649P.	
PR	20-MAR-1998;	98US-0078886P.	
PR	20-MAR-1998;	98US-0078939P.	
PR	27-MAR-1998;	98US-0079664P.	
PR	27-MAR-1998;	98US-0079786P.	
PR	31-MAR-1998;	98US-0080107P.	
PR	31-MAR-1998;	98US-0080194P.	
PR	01-APR-1998;	98US-0080327P.	
PR	01-APR-1998;	98US-0080333P.	
PR	08-APR-1998;	98US-0081049P.	
PR	08-APR-1998;	98US-0081070P.	
PR	09-APR-1998;	98US-0081195P.	
PR	15-APR-1998;	98US-0081838P.	
PR	21-APR-1998;	98US-0082568P.	
PR	21-APR-1998;	98US-0082569P.	
PR	22-APR-1998;	98US-0082704P.	
PR	22-APR-1998;	98US-0082797P.	
PR	28-APR-1998;	98US-0083322P.	
PR	29-APR-1998;	98US-0083495P.	
PR	29-APR-1998;	98US-0083496P.	
PR	29-APR-1998;	98US-0083499P.	
PR	29-APR-1998;	98US-0083559P.	
PR	05-MAY-1998;	98US-0083436P.	
PR	06-MAY-1998;	98US-0084414P.	
PR	07-MAY-1998;	98US-0084639P.	
PR	07-MAY-1998;	98US-0084640P.	
PR	07-MAY-1998;	98US-0084643P.	
PR	15-MAY-1998;	98US-0085579P.	
PR	15-MAY-1998;	98US-0085580P.	
PR	15-MAY-1998;	98US-0085582P.	
PR	15-MAY-1998;	98US-0085700P.	
PR	18-MAY-1998;	98US-0086023P.	
PR	22-MAY-1998;	98US-0086392P.	
PR	22-MAY-1998;	98US-0086486P.	
PR	28-MAY-1998;	98US-0087098P.	
PR	28-MAY-1998;	98US-0087208P.	
PR	02-JUN-1998;	98US-0087609P.	
PR	02-JUN-1998;	98US-0087759P.	
PR	03-JUN-1998;	98US-0087827P.	
PR	04-JUN-1998;	98US-0088025P.	
PR	04-JUN-1998;	98US-0088028P.	
PR	04-JUN-1998;	98US-0088039P.	
PR	04-JUN-1998;	98US-0088033P.	
PR	04-JUN-1998;	98US-0088326P.	
PR	05-JUN-1998;	98US-0088167P.	
PR	05-JUN-1998;	98US-0088202P.	
PR	05-JUN-1998;	98US-0088212P.	
PR	05-JUN-1998;	98US-0088217P.	

RESULT 13
ABU58409
ID ABU58409 standard; protein; 382 AA.
XX
AC AC
XX XX
DT 15-APR-2003 (first entry)
XX XX
DE Human PRO polypeptide #10.
XX XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrg therapy.
XX XX
OS Homo sapiens.
XX XX
PN US2003027272-A1.
XX XX
PD 06-FEB-2003.
XX XX

PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
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PR 10-JUN-1998; 98US-0088826P.
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PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
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PR 16-SEP-1998; 98WO-US01330.
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PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
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PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 98.7%; Score 1086; DB 6; Length 382;

Best Local Similarity 96.2%; Pred. No. 3.7e-102;

Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

Qy 1 RLLS-----GQPVCRGGTORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI ESE 52
Db 25 RLLSASDLRLRGQPVCRGGTORPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI ESE 84
Qy 53 DEQKLEKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
Db 85 DEQKLEKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144
Qy 113 CGSEVCVMYHQPSAPAGIGGYPYMFQWNNDRCNMKNNFICKYSDEKPAVPSREAEGETE 172
Db 145 CGSEVCVMYHQPSAPAGIGGYPYMFQWNNDRCNMKNNFICKYSDEKPAVPSREAEGETE 204
Qy 173 LTTPLPEETQEDAKKTFKESREAAALNLAY 203
Db 205 LTTPLPEETQEDAKKTFKESREAAALNLAY 235

RESULT 14

ABU71613

ID ABU71613 standard; protein; 382 AA.

XX AC ABU71613;

XX DT 16-JUN-2003 (first entry)

XX DE Human PRO polypeptide #24.

XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW patholological disorder; cardiac insufficiency disorder; protein secretion;
KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;

KW cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal;
XW antiulcer; dermatological; vulnerary.
XX

OS Homo sapiens.

PN US2002146709-A1.

XX 10-OCT-2002.

XX 18-JUL-2001; 2001US-00909088.

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

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PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

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PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 17-NOV-1997; 97US-0065846P.

PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.

PR 21-NOV-1997; 97US-0066364P.

PR 24-NOV-1997; 97US-0066453P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066511P.

PR 24-NOV-1997; 97US-0066770P.

PR 24-NOV-1997; 97US-0066772P.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 01-DEC-1998; 98WO-US025108.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Deanoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2003-328338/31.
DR N-PSDB; ACA59008.
XX
PT Isolated nucleic acid useful for e.g., treating pathological disorders
PT encodes a secreted or transmembrane protein.
XX
PS Claim 12; Fig 50; 473pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted or
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC PRO polypeptides and polynucleotides can be used in treating pathological
CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
CC disorders and in therapeutic treatment of disorders involving protein
CC secretion by the pancreas, including diabetes. They can also be used in
CC treating disorders associated with the preservation and maintenance of
CC gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, and skin diseases associated with abnormal keratinocyte
CC differentiation (e.g., psoriasis, epithelial cancers such as lung
CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
CC The sequences can be used as molecular markers for protein
CC electrophoresis purposes and can be utilised in protein-protein binding
CC assays, biochemical screening assays, immunoassays and cell-based assays.
CC This sequence represents a human PRO polypeptide of the invention
XX
SQ Sequence 382 AA;

Query Match 98.7%; Score 1086; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.7e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKACRRDGGQLVSI 52
Db |||||
25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRRLNFEEAKACRRDGGQLVSI 84
QY 53 DEQKLIKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
Db |||||
85 DEQKLIKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144
QY 113 CGSEVVCVMYHQPSPAPAGIGGPFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 172
Db |||||
145 CGSEVVCVMYHQPSPAPAGIGGPFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 204
QY 173 LTTPLPEETQEDAKKTFKESREALNLAY 203
Db |||||
205 LTTPLPEETQEDAKKTFKESREALNLAY 235

RESULT 15
ABU87957
ID ABU87957 standard; protein; 382 AA.
XX
AC ABU87957;
XX
DT 07-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO234.
XX
KW Human; secreted and transmembrane protein: PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
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PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
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PR 17-AUG-1998; 98US-0096757P.
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PR 26-AUG-1998; 98US-0097954P.
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PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
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PR 16-SEP-1998; 98US-0101751P.
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PR 17-SEP-1998; 98US-0100683P.
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PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
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PR 25-SEP-1998; 98US-0101786P.
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PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.

Query Match 98.7%; Score 1086; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.7e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
1 RLIS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLYSIESE 52
25 RLISASDLDRGGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLYSIESE 84
53 DEQKLEKFIENLLPSDGDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNWIYDEPS 112
85 DEQKLEKFIENLLPSDGDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNWIYDEPS 144
113 CGSEVCVMYHQPAPAGIGGPMFQWDDRCNMKNFNICKYSDEKPAVPSREAEGETE 172
145 CGSEVCVMYHQPAPAGIGGPMFQWDDRCNMKNFNICKYSDEKPAVPSREAEGETE 204

QY 173 LTPVLPEETQEDAKTKFKESREAAALNLAY 203
Db 205 LTPVLPEETQEDAKTKFKESREAAALNLAY 235
RESULT 16
ABU84272
ID ABU84272 standard; protein; 382 AA.
XX
AC ABU84272;
XX
XX 02-AUG-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) #10.
KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032112-A1.
XX PD
XX 13-FEB-2003.
PF 21-JUN-2002; 2002US-00176756.
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
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PR 01-APR-1998; 98US-0080327P.
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PR 08-APR-1998; 98US-0081049P.
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PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
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PR 22-APR-1998; 98US-0082797P.
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Best Local Similarity 96.2%; Pred.No.3.7e-102;

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RESULT 17
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AC ABR66146;
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DT 05-AUG-2003 (first entry)
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KW extracellular domain; tumour necrosis factor-alpha; cartilage disorder;
KW chondrocyte; proliferation; differentiation; cancer; tumour; diagnosis;
KW bone disorder; arthritis; sports injury; kidney; rectum; cervix;
KW adrenal tumour; lung; colon; breast; prostate; kidney; genetic analysis;
KW liver; drug screening; transgenic animal; gene therapy.
KW antiarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027278-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176987.
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98.7%; Score 1086; DB 6; Length 382;

Best Local Similarity 96.2%; Pred. No. 3.7e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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RESULT 19
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ID ABU99476 standard; protein; 382 AA.
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AC ABU99476;
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DT 09-AUG-2003 (first entry)
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DE Human secreted/transmembrane protein (PRO) #10.
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KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
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Qy	53	DEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNMYVDEPS
Db	85	DEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNMYVDEPS
Qy	113	CGSEVCVMYHQSPAPAGIGGPFYMFQWNNDRRCNMKNFICKYSDEKPAVPSREAEGETE
Db	145	CGSEVCVMYHQSPAPAGIGGPFYMFQWNNDRRCNMKNFICKYSDEKPAVPSREAEGETE
Qy	173	LTPVLPEETOEDAKKTFKESREAAALNLAY
Db	205	LTPVLPEETOEDAKKTFKESREAAALNLAY
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XX	10-JUN-2003 (first entry)	
DE	Human PRO polypeptide #24.	
KW	Human; secreted and transmembrane protein; PRO polypeptide; cancer;	
KW	Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;	
XX	neuroprotective.	
OS	Homo sapiens.	
XX	US2002192659-A1.	
PD	19-DEC-2002.	
XX	10-JUL-2001; 2001US-00902853.	
XX	17-SEP-1997; 97US-0059113P.	
PR	17-SEP-1997; 97US-0059115P.	
PR	17-SEP-1997; 97US-0059117P.	
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PR	18-SEP-1997; 97US-0059263P.	
PR	18-SEP-1997; 97US-0059266P.	
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PR 03-NOV-1997; 97US-0064248P.
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PR 12-NOV-1997; 97US-0065186P.
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PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
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PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
XX PA
XX PI
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-361832/34.

DR N-PSDB; ACA58405.
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 12; Fig 50; 474pp; English.
XX
CC The present invention relates to the isolation of novel human secreted
CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
CC sequences encoding them. The polynucleotide sequences are useful in
CC molecular biology, as hybridisation probes, in chromosome and gene
CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide sequences may also be used in preparing PRO polypeptides
CC by recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptides or
CC their antibodies are useful in preparing a medicament for treating a
CC condition responsive to the polypeptide or antibody, such as cancer,
CC Alzheimer's disease or ischaemia, and in various diagnostic assays.
CC ABU71445-ABU71505 represent human PRO polypeptides of the invention
XX
SQ Sequence 382 AA;

Query Match 98.7%; Score 1086; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.7e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
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QY 53 DEQKLIEXFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSI 112
Db |||||
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QY 113 CGSEVCVVMYHQPSAPAGIGGPMFQWDDRCNMKNFKICKYDEKPAVPSREAE 172
Db |||||
145 CGSEVCVVMYHQPSAPAGIGGPMFQWDDRCNMKNFKICKYDEKPAVPSREAE 204

QY 173 LTPVLPETQEEDAKTKFKESREAAINLAY 203
Db |||||
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RESULT 23
ABR68085
ID ABR68085 standard; protein; 382 AA.
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AC ABR68085;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO234, SEQ ID NO:20.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
FN US2003027264-A1.
XX
PD 06-FEB-2003.
XX
PF 18-JUN-2002; 2002US-00174579.
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PR 18-SEP-1997; 97US-0059263P.
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PR 17-OCT-1997; 97US-0062250P.
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Best Local Similarity 96.2%; Pred. No. 3.7e-102;
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DT 18-JUL-2003 (first entry)

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KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cell; TNF-alpha;
KW tumour necrosis factor-alpha; gene therapy.

XX
OS Homo sapiens.

XX
PN US2003036149-A1.

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Query Match

Best Local Similarity

Matches 203; Conservative

98.7%;

Score 1086;

DB 6;

Length 382;

96.2%;

Pred.No.3.7e-102;

0;

Mismatches

0;

Indels

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Gaps

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Qy	173	LTPVLPEETQEDAKKTFKESREAAALNLAY	203
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:47:24 ; Search time 71.8231 Seconds
(without alignments)
891.777 Million cell updates/sec

Title: US-09-887-855-2_COPY_25_227
Perfect score: 1100
Sequence: 1 RLLSGQPVCRGGTQPCYKV.....EEDAKTFKESREALNLAY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_irvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1100	100.0	374	4 Q96NF3	Q96nf3 homo sapien
3	1096	99.6	374	4 Q96NC5	Q96nc5 homo sapien
4	939.5	85.4	374	11 Q9Z209	Q9z209 cricetulus
5	797.5	72.5	211	11 Q8C351	Q8c351 mus musculus
6	580	52.7	246	11 Q8BVI7	Q8bvi7 mus musculus
7	580	52.7	292	11 Q8BVU2	Q8bvu2 mus musculus
8	513	46.6	236	4 Q7Z798	Q7z798 homo sapien
9	504.5	45.9	232	4 Q7Z799	Q7z799 homo sapien
10	500	45.5	236	4 Q7Z7A0	Q7z7a0 homo sapien
11	185	16.8	1290	13 Q9W6E1	Q9w6e1 gallus gall
12	178.5	16.2	1456	11 Q61830	Q61830 mus musculus
13	177.5	16.1	1348	5 Q25199	Q25199 hydra atten
14	176.5	16.0	1479	4 Q9Y5P9	Q9y5p9 homo sapien
15	176.5	16.0	1479	4 Q9UBG0	Q9ubg0 homo sapien
16	170.5	15.5	1479	11 Q64449	Q64449 mus musculus

17	169	15.4	217	11	Q8C4F8	Q8c4f8 mus musculu
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19	165.5	15.0	742	11	Q8C979	Q8c979 mus musculu
20	161.5	14.7	134	5	Q9XYX3	Q9xyx3 hydra magni
21	159.5	14.5	742	11	Q8VIF6	Q8vif6 mus musculu
22	158	14.4	142	11	Q8CJ86	Q8cj86 mus musculu
23	158	14.4	142	11	Q8BHK7	Q8bhk7 mus musculu
24	158	14.4	295	11	Q91ZW4	Q91zw4 mus musculu
25	158	14.4	311	11	Q9D8V4	Q9d8v4 mus musculu
26	158	14.4	325	11	Q91ZX0	Q91zx0 mus musculu
27	157	14.3	158	13	Q90WI7	Q90wi7 bungarus fa
28	156	14.2	323	11	Q8CJ91	Q8cj91 mus musculu
29	156	14.2	339	6	Q95244	Q95244 sus scrofa
30	155	14.1	293	11	Q8BGZ0	Q8bgz0 mus musculu
31	155	14.1	323	11	Q8CJ94	Q8cj94 mus musculu
32	155	14.1	323	11	Q8CJ93	Q8cj93 mus musculu
33	155	14.1	323	11	Q8CJ88	Q8cj88 mus musculu
34	155	14.1	379	11	Q7TMA7	Q7tma7 mus musculu
35	155	14.1	473	11	Q7TSP9	Q7tsp9 mus musculu
36	155	14.1	477	11	Q7TSQ7	Q7tsq7 mus musculu
37	155	14.1	504	11	Q7TSQ0	Q7tsq0 mus musculu
38	155	14.1	534	11	Q7TSQ1	Q7tsq1 mus musculu
39	155	14.1	1152	13	Q90WM2	Q90wm2 xenopus lae
40	154	14.0	322	11	Q8CJ89	Q8cj89 mus musculu
41	154	14.0	323	11	Q8CJ92	Q8cj92 mus musculu
42	153	13.9	446	4	Q7Z5K9	Q7z5k9 homo sapien
43	152.5	13.9	485	6	Q95LG3	Q95lg3 odocoileus
44	152	13.8	158	13	Q90WI6	Q90wi6 bungarus mu
45	151.5	13.8	652	4	Q8IXK1	Q8ixk1 homo sapien

ALIGNMENTS

RESULT 1
Q8TAY8
ID Q8TAY8 PRELIMINARY; PRT; 374 AA.
AC Q8TAY8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to unnamed protein product.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025407; AAH25407.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
SQ SEQUENCE 374 AA; 42312 MW; FC214E6BC9E578D9 CRC64;

Query Match	100.0%;	Score	1100;	DB	4;	Length	374;
Best Local Similarity	100.0%;	Pred. No.	1.2e-97;				
Matches	203;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
QY	1	RLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI	EDEQKLI	EK	60		
Db	25	RLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI	EDEQKLI	EK	84		
QY	61	FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSI	SQFRN	WYVDEP	SCGSEVCV	120	
Db	85	FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSI	SQFRN	WYVDEP	SCGSEVCV	144	
QY	121	MYHQSPAPAGIGGYMFQWDDRCNMKNFKCKYSDEKPAVPSREAE	GHE	TELT	TPVLP	180	

Db 145 MYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204
 QY 181 ETQEDAKKTFKESREAAALNLAY 203
 Db 205 ETQEDAKKTFKESREAAALNLAY 227

RESULT 2

Q96NF3
 ID Q96NF3 PRELIMINARY; PRT; 374 AA.
 AC Q96NF3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ30977.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
 RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Chiba Y.,
 RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK055539; BAB70946.1; -;
 DR GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 374 AA; 42280 MW; 8AE64E6BC9E56DCD CRC64;

Query Match 100.0%; Score 1100; DB 4; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.2e-97;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLIK 60
 Db 25 RLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLIK 84
 QY 61 FIENLLPSDGFWICLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
 Db 85 FIENLLPSDGFWICLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 144
 QY 121 MYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
 Db 145 MYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204
 QY 181 ETQEDAKKTFKESREAAALNLAY 203
 Db 205 ETQEDAKKTFKESREAAALNLAY 227

RESULT 3

Q96NC5
 ID Q96NC5 PRELIMINARY; PRT; 374 AA.
 AC Q96NC5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ31092.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]
 RP SEQUENCE FROM N.A.
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
 RA Isogai T.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK055654; BAB70978.1; -;
 DR GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 374 AA; 42310 MW; CBF74E676E23BA16 CRC64;

Query Match 99.6%; Score 1096; DB 4; Length 374;
 Best Local Similarity 99.5%; Pred. No. 2.9e-97;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLIK 60
 Db 25 RLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSISEDEQKLIK 84
 QY 61 FIENLLPSDGFWICLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
 Db 85 FIENLLPSDGFWICLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 144
 QY 121 MYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
 Db 145 MYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204
 QY 181 ETQEDAKKTFKESREAAALNLAY 203
 Db 205 ETQEDAKKTFKESREAAALNLAY 227

RESULT 4

Q9Z209
 ID Q9Z209 PRELIMINARY; PRT; 374 AA.
 AC Q9Z209;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Layilin.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 CX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Borowsky M.L., Hynes R.O.;
 RT "Layilin, a novel talin-binding transmembrane protein homologous with
 RT C-type lectins, is localized in membrane ruffles."
 RL J. Cell Biol. 143:0-0(1998).
 DR EMBL; AF093673; AAC68695.1; -;
 DR HSSP; P22897; 1EGG.
 DR GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 SQ SEQUENCE 374 AA; 42435 MW; 298A8EA24FB04E1C CRC64;
 Query Match 85.4%; Score 939.5; DB 11; Length 374;
 Best Local Similarity 85.8%; Pred. No. 3.5e-82;

QY	1	RLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSI	60	DEQKLIK	60
Db	25	RLSGQLVCRGGTRRRCYKVIYFHDFAFQRLNFEAEKACRRDGGQLVSI	84	DEQRLIK	84
QY	61	FIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRN	120	WVDEPSCGSEVCV	120
Db	85	FIENLLASDGFWIGLRRLEVKQVNTACQDLYAWTDGSIQFRN	144	WVDEPSCGSEVCV	144
QY	121	MYHQSAPAGIGGPFQWQNDRCNMKNFICKYSDEKPA-VPSRA	179	EAEGEETLTPVLP	179
Db	145	MYHQSAPPGIGGSYMFQWQNDRCNMKNFICKYADEKPS	204	TPPGATEPPTPVL	204
QY	180	EETQEDAKTKFESREAAALNAY	203		
Db	205	EETQKEDTKETFKESREAAALNAY	228		
RESULT 5					
Q8C351	ID	Q8C351	PRELIMINARY;	PRT;	211 AA.
AC	Q8C351;				
DT	01-MAR-2003	(TReMBLrel. 23, Created)			
DT	01-MAR-2003	(TReMBLrel. 23, Last sequence update)			
DT	01-OCT-2003	(TReMBLrel. 25, Last annotation update)			
DE	LAYILIN	homolog (Fragment).			
OS	Mus musculus	(Mouse).			
OC	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria;	Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J;	TISSUE=Lung;			
RX	MEDLINE=22354683;	PubMed=12466851;			
RA	The FANTOM Consortium,				
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of				
RT	60,770 full-length cDNAs."				
RL	Nature 420:563-573 (2002).				
DR	EMBL; AK086930;	BAC39765.1; --			
DR	GO: 0005529;	F:sugar binding; IEA.			
DR	InterPro; IPR001304;	Lectin_C.			
DR	Pfam; PF00059;	lectin_c; 1.			
DR	SMART; SM00034;	CLECT; 1.			
DR	PROSITE; PS50041;	C TYPE LECTIN_2; 1.			
FT	NON TER	211			
SQ	SEQUENCE	211 AA; 23697 MW; AD9870B5957DD5AE	CRC64;		
Query Match 72.5%; Score 797.5; DB 11; Length 211;					
Best Local Similarity 79.7%; Pred. No. 8.4e-69;					
Matches 149; Conservative 9; Mismatches 20; Indels 9; Gaps 2;					
QY	1	RLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSI	52	ESE	52
Db	25	RLLSASDLDPGGQLVCRGGTRRRCYKVIYFHDFAFQRLNFEAEKAC	84	TCMEDGGQLVSIETE	84
QY	53	DEQKLIKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRN	112	WVDEPS	112
Db	85	DEQRLIKFIENLLASDGFWIGLKRLEEKQSNNTACQDLYAWTDGSIQFRN	144	WVDEPS	144
QY	113	CGSEVCVMYHQSAPAGIGGPFQWQNDRCNMKNFICKYSDEKPA-VPSRA	171	EAEGEET	171
Db	145	CGSEVCVMYHQSAPPGIGGSYMFQWQNDRCNMKNFICKYHDDKPS	204	TPPGGEAT	204
QY	172	ELTTPVL	178		
Db	205	EPATPLL	211		
RESULT 6					
Q8BMI7	ID	Q8BMI7	PRELIMINARY;	PRT;	246 AA.
AC	Q8BMI7;				

DT	01-MAR-2003	(TReMBLrel. 23, Created)			
DT	01-MAR-2003	(TReMBLrel. 23, Last sequence update)			
DT	01-OCT-2003	(TReMBLrel. 25, Last annotation update)			
DE	C-type lectin protein	MT75 homolog.			
GN	CHODL.				
OS	Mus musculus	(Mouse).			
OC	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria;	Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J;	TISSUE=Forelimb;			
RX	MEDLINE=22354683;	PubMed=12466851;			
RA	The FANTOM Consortium,				
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of				
RT	60,770 full-length cDNAs."				
RL	Nature 420:563-573 (2002).				
DR	EMBL; AK031063;	BAC27234.1; --			
DR	MGD; MGI:2179069;	Chodl.			
DR	GO: 0005529;	F:sugar binding; IEA.			
DR	InterPro; IPR001304;	Lectin_C.			
DR	Pfam; PF00059;	lectin_c; 1.			
DR	SMART; SM00034;	CLECT; 1.			
DR	PROSITE; PS50041;	C TYPE LECTIN_2; 1.			
SQ	SEQUENCE	246 AA; 27394 MW; E872660C58267752	CRC64;		
Query Match 52.7%; Score 580; DB 11; Length 246;					
Best Local Similarity 57.9%; Pred. No. 9.3e-48;					
Matches 110; Conservative 26; Mismatches 40; Indels 14; Gaps 5;					
QY	1	RLSGQPVCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSI	60	DEQKLIK	60
Db	23	RVVSGQKVCFAADVHKPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSI	82	DEQKLIK	82
QY	61	FIENLLP-----SDGDFWIGLRRREKQSNSTACQDLYAWTDGSIQFRN	115	WVDEPSCGS	115
Db	83	MLQNLTKPGTGISDGFWIGLRRSGDQT-SGACPDLYQWSDGSSSQFRN	141	WVDEPSCGS	141
QY	116	EVCVMYHQSAPAGIGGPFQWQNDRCNMKNFICKYSDE-KPAVPSRA	174	EAEGEETELT	174
Db	142	EKCVVMYHQTANPGLGGPYLYQWQNDRCNMKNFICKYEPHTEPA	196	-----EKP	196
QY	175	TPVLPEETQE	184		
Db	197	NQ--PEETHE	204		
RESULT 7					
Q8BVU2	ID	Q8BVU2	PRELIMINARY;	PRT;	292 AA.
AC	Q8BVU2;				
DT	01-MAR-2003	(TReMBLrel. 23, Created)			
DT	01-MAR-2003	(TReMBLrel. 23, Last sequence update)			
DT	01-OCT-2003	(TReMBLrel. 25, Last annotation update)			
DE	C-type lectin protein	MT75 homolog.			
GN	CHODL.				
OS	Mus musculus	(Mouse).			
OC	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria;	Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J;	TISSUE=Head;			
RX	MEDLINE=22354683;	PubMed=12466851;			
RA	The FANTOM Consortium,				
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of				
RT	60,770 full-length cDNAs."				
RL	Nature 420:563-573 (2002).				
DR	EMBL; AK076523;	BAC36378.1; --			
DR	MGD; MGI:2179069;	Chodl.			
DR	GO: 0005529;	F:sugar binding; IEA.			

RESULT 11
Q9W6E1 PRELIMINARY; PRT; 1290 AA.
AC Q9W6E1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Neurocan core protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20309833; PubMed=10851024;
RA Li H., Leung T.C., Hoffman S., Balsamo J., Lilien J.;
RT "Coordinate Regulation of Cadherin and Integrin Function by the
RT Chondroitin Sulfate Proteoglycan Neurocan."
RL J. Cell Biol. 149:1275-1288(2000).
DR EMBL; AF116856; AAD24546.2; -.
DR HSSP; P08709; 1BF9.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; xlink; 2.
DR PRINTS; PR0010; EGFLOOD.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00515; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1_2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW EGF-like domain.
SQ SEQUENCE 1290 AA; 138877 MW; 182BD86D0E40BE78 CRC64;
Query Match 16.8%; Score 185; DB 13; Length 1290;
Best Local Similarity 34.7%; Pred.No. 8.1e-09;
Matches 50; Conservative 18; Mismatches 42; Indels 34; Gaps 8;
QY 14 QRPCYKVIYFHDTSRRLNFEAEKACRRDGGQGLVSI ESEDEQKLIKFIENLLPSDGD^{FW} 73
DB 1064 QGHCYR--YF---SRRRSWEDAERDCRRRAGHLTSHSQEEHGFINSF-----GHENTW 1112
QY 74 IGLRREEKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPS---CGSEVCVVMY-HQPSAPA 129
DB 1113 IGLNDRIVEQD-----FQWTDNTGLQYENWRENQPNFPAGGEDCVVLVSHE----- 1159

QY 130 GIGGPFMFQWDDRCNMKNMFICK 153
DB 1160 -IG-----KWNDVPCNYNLPYICK 1177
RESULT 12
Q61830 PRELIMINARY; PRT; 1456 AA.
AC Q61830;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Macrophage mannose receptor precursor.
GN MRC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=93043353; PubMed=1421407;
RA Harris N., Rits M., Chang G., Ezekowitz R.B.;
RT "Characterization of the murine macrophage mannose receptor."
RL Blood 80:2363-2373(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Super M.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z11974; CAA78028.1; -.
DR PIR; A48925; A48925.
DR PDB; 1DQG; 10-MAY-00.
DR PDB; 1DQO; 10-MAY-00.
DR PDB; 1FWU; 17-JAN-01.
DR PDB; 1FWV; 17-JAN-01.
DR MGD; MGI:97142; Mrc1.
DR GO; GO:0009928; C:cell surface (sensu Magnoliophyta); IDA.
DR GO; GO:0005537; F:mannose binding; IDA.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR008997; RicinB_like.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin_c; 8.
DR Pfam; PF00652; Ricin_B_lectin; 2.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PD00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 6.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS50231; RICIN_B_LLECTIN; 1.
KW Receptor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1456 MACROPHAGE MANNOSE RECEPTOR.
SQ SEQUENCE 1456 AA; 165065 MW; 4EBD3F1B8619A594 CRC64;
Query Match 16.2%; Score 178.5; DB 11; Length 1456;
Best Local Similarity 25.9%; Pred.No. 4e-08;
Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;
QY 18 YKVIYFHDTSRRLNFEAEKACRRDGGQGLVSI ESEDEQKLIKFIENLLPSDGD^{FW}IGLR 77
DB 807 YKDYQYFFSKEKETMDNARRCKKNGFDLTIKSESEKKFLWKYL-NKNGGQSPYFIGML 865
QY 78 RREEKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY 135

Db 866 ISMDKK-----FIWMDGSKVDFAVATGEPNPFANDDENCVTMY-----TNSGF---- 908
 QY 136 MFQWDDRCNMKNFICK--YSDEKPAVPSREAEGETELTTPVLPEETOE----- 184
 Db 909 ---WNDINGYPNNFICORHSSINATAMP-----TTPTPGCKEGWHLYKNK 954
 QY 185 -----EDAKKTFKESREAAALNL 201
 Db 955 CFKIFGFANEKKSWQDARQACKGL 979

RESULT 13
 Q25199 ID Q25199 PRELIMINARY; PRT; 1348 AA.
 AC Q25199;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
 DE Tyrosine kinase receptor.
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Anthomedusae;
 OC Hydridae; Hydra.
 OX NCBI_TaxID=6087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Irvine;
 RX MEDLINE=20209407; PubMed=10744720;
 RA Reidling J.C., Miller M.A., Steele R.E.;
 RT "Sweet Tooth, a Novel Receptor Protein-tyrosine Kinase with C-type
 RT Lectin-like Extracellular Domains";
 RL J. Biol. Chem. 275:10323-10330(2000).
 DR EMBL; L22612; AAA29218.2; -.
 DR HSSP; P11362; 1FGK.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001304; LECTIN_C.
 DR InterPro; IPR003990; Pancreatins_ac.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF00059; lectin_c; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR01504; PNCREATITSAP.
 DR ProDom; PD000001; Prot_kinase; 2.
 DR SMART; SM00034; CLECT; 4.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 2.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 4.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 1348 AA; 156916 MW; 77D2122093227FEF CRC64;

Query Match 16.1%; Score 177.5; DB 5; Length 1348;
 Best Local Similarity 28.0%; Pred. No. 4.5e-08;
 Matches 47; Conservative 32; Mismatches 46; Indels 43; Gaps 8;
 QY 3 LSGQPVC--RGGTQPC-----YKVIYFHDTSRLNPFEEAKEACRRDGGQLVSISEDE 54
 Db 412 LSHRFICKVKRATNEYCAEGWTSYRIYCFIYSIEFDWFKSFSCQNGNLLSIENOE 471
 QY 55 QKLEKFIENLLPSDGD-FWIGLRR-----REEKQSNSTACQDLYAWTDGSIQFRNMY 107
 Db 472 ----NRFIENDLIKNDKDWIGLKIWNIDYLNKKNR-----FEWSDNTYTQFFNWI 518
 QY 108 VDEP--SCGSEVCVVMYHQPAPAGIGPYPMFQWDDRCNMKNFNICK 153
 Db 519 TNQPDNNNGIESCVEMNYN-----GWSDKCKVLDNGFICK 553

RESULT 14
 Q9Y5P9 ID Q9Y5P9 PRELIMINARY; PRT; 1479 AA.
 AC Q9Y5P9;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
 DE Endocytic receptor Endo180.
 GN ENDO180.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20148849; PubMed=10683150;
 RA Sheikh H., Yarwood H., Ashworth A., Isacke C.;
 RT "Endo180, an endocytic recycling glycoprotein related to the
 RT macrophage mannose receptor is expressed on fibroblasts, endothelial
 RT cells and macrophages and functions as a lectin receptor.";
 RL J. Cell Sci. 113:1021-1032(2000).
 DR EMBL; AF134838; AAD30280.1; -.
 DR HSSP; P02751; 2FN2.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR001304; LECTIN_C.
 DR InterPro; IPR000566; Lipocln_cytFABP.
 DR InterPro; IPR008997; RicinB_like.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR Pfam; PF00040; fn2; 1.
 DR Pfam; PF00059; lectin_c; 8.
 DR PRINTS; PR00013; FNTYPEII.
 DR ProDom; PD000995; FN_Type_II; 1.
 DR SMART; SM00034; CLECT; 8.
 DR SMART; SM00059; FN2; 1.
 DR SMART; SM00458; RICIN; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 3.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 8.
 DR PROSITE; PS00023; FIBRONECTIN_2; 1.
 DR PROSITE; PS00213; LIPOCALIN; 1.
 DR PROSITE; PS50231; RICIN_B_LLECTIN; 1.
 KW Receptor.
 SQ SEQUENCE 1479 AA; 166669 MW; 9F4BAF355F036FCE CRC64;

Query Match 16.0%; Score 176.5; DB 4; Length 1479;
 Best Local Similarity 30.4%; Pred. No. 6.3e-08;
 Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;
 QY 4 SGQPVCRGGTQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSISEDEQKLEKFI 63
 Db 385 SWQPF-----QGHCVRL-----QAEKRSWQESKKACLRGGGDLVSIHSMAELEFITKQIK 434
 QY 64 NLLPSDGDGDFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNMYVDEPS---CGSEVCV 120
 Db 435 QEVE---ELWIGL-----NDLKLQMNFEWSGSLVSFTHWPFEPNFRDSDLEDCVT 483
 QY 121 MYHQSPAPAGIGPYPMFQWDDRCNMKNFNICKYSDEKPAVPSREAE 168
 Db 484 IW----GPEG-----RWNDSPCNQSLPSICKKAGQLSQGAAEHDHG 520

RESULT 15
 Q9UBGO ID Q9UBGO PRELIMINARY; PRT; 1479 AA.
 AC Q9UBGO;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)

DE Urokinase receptor-associated protein UPARAP.
GN KIAA0709.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Behrendt N., Jensen O.N., Engelholm L.H., Mortz E., Mann M., Dano K.;
RT "A urokinase receptor-associated protein with specific collagen-
RT binding properties.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
DR EMBL; AF107292; AAF14192.1; -.
DR EMBL; AB014609; BAA31684.1; -.
DR HSSP; P02751; 2FN2.
DR Genew; HGNC:16875; MRC2.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR008997; RicinB_Like.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin_c; 8.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 3.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS50231; RICIN_B_LECTIN; 1.
KW Kinase; Receptor.
SQ SEQUENCE 1479 AA; 166654 MW; C7583EA78E2792D1 CRC64;

Query Match 16.0%; Score 176.5; DB 4; Length 1479;
Best Local Similarity 30.4%; Pred. No. 6.3e-08;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;

QY 4 SGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKEACRRDGGQLVSI ESEDEQKLIK FIE 63
Db 385 SWQPF-----QGH CYRL-----QA EKRSWQESKKACLRGGDLVSIHSM AELEFITKQIK 434

QY 64 NLLPSDGD F WIGLR RREKQSNSTACQDLYAWTDGSI SQFRN WYVDEPS---CGSEVCV V 120
Db 435 QEVE---ELWIGL-----NDLKLQMNFEWSDGSLVSFTHWHPFEPNFRD SLEDCVT 483

QY 121 MYHQPSAPAGIGGPFYMFQWNDRCNMKNFICKYSDEKPAVPSREAG 168
Db 484 IW-----GPEG-----RWNDSPCNQSLPSICKKAGQLSQGA AEEDHG 520

RESULT 16
Q64449
ID Q64449 PRELIMINARY; PRT; 1479 AA.
AC Q64449;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lectin lambda.
GN MRC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96355501; PubMed=8702911;
RA Wu K., Yuan J., Lasky L.A.;
RT "Characterization of a novel member of the macrophage mannose receptor
RT type C lectin family.";
RL J. Biol. Chem. 271:21323-21330(1996).
DR EMBL; U56734; AAC52729.1; -.
DR PIR; T42710; T42710.
DR HSSP; P02751; 2FN2.
DR MGD; MGI:107818; Mrc2.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR008997; RicinB_Like.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00059; lectin_c; 8.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 1.
DR SMART; SM00034; CLECT; 8.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00458; RICIN; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 3.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 8.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS50231; RICIN_B_LECTIN; 1.
SQ SEQUENCE 1479 AA; 167112 MW; 62D456E10B9B48C1 CRC64;

Query Match 15.5%; Score 170.5; DB 11; Length 1479;
Best Local Similarity 31.4%; Pred. No. 2.4e-07;
Matches 48; Conservative 22; Mismatches 48; Indels 35; Gaps 7;

QY 4 SGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKEACRRDGGQLVSI ESEDEQKLIK FIE 63
Db 384 SWQPF-----QGH CYRL-----QA EKRSWQESKKACLRGGDLVSIHSM AELEFITKQIK 433

QY 64 NLLPSDGD F WIGLR RREKQSNSTACQDLYAWTDGSI SQFRN WYVDEPS---CGSEVCV V 120
Db 434 QEVE---ELWIGL-----NDLKLQMNFEWSDGSLVSFTHWHPFEPNFRD SLEDCVT 482

QY 121 MYHQPSAPAGIGGPFYMFQWNDRCNMKNFICK 153
Db 483 IW-----GPEG-----RWNDSPCNQSLPSICK 504

RESULT 17
Q8C4F8
ID Q8C4F8 PRELIMINARY; PRT; 217 AA.
AC Q8C4F8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chondroitin sulfate proteoglycan 3 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 20
Q9XYX3
ID Q9XYX3 PRELIMINARY; PRT; 134 AA.
AC Q9XYX3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Receptor protein-tyrosine kinase (Fragment).
GN HTK28.
OS Hydra magnipapillata (Hydra).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RX MEDLINE=20209407; PubMed=10744720;
RA Reidling J.C., Miller M.A., Steele R.E.;
RT "Sweet Tooth, a Novel Receptor Protein-tyrosine Kinase with C-type
RT Lectin-like Extracellular Domains."
RL J. Biol. Chem. 275:10323-10330(2000).
DR EMBL; AF129528; AAD30040.1; -.
DR HSSP; P22897; 1EGG.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:000529; F:sugar binding; IEA.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Kinase; Tyrosine-protein kinase.
FT NON_TER 1
FT NON_TER 134
FT NON_TER 134
SQ SEQUENCE 134 AA; 15701 MW; E7B7211C881009BC CRC64;

Query Match 14.7%; Score 161.5; DB 5; Length 134;
Best Local Similarity 28.8%; Pred. No. 9.8e-08;
Matches 40; Conservative 23; Mismatches 51; Indels 25; Gaps 5;

QY 17 CYKVIYFHDTSRRLNFEAEKACRRDGGQLVSISEDEQKLIKFIENLLPSDGFWIGL 76
Db 16 CY--FFQNTLQAKNWRDASLSCQALGHLISIEDQAENFFILNFKDSSMQDNYWIGL 73

QY 77 RRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS--CGSEVCVVMYHQPSPAPAGIGGP 134
Db 74 -----NDASNNREFRWSDDKIPQFFNWLPRKPNNDQSEQNCV-----ETNSMG-- 116

QY 135 YMFQWNDRCNMKNFICK 153
Db 117 ----WNDENCDAATNGFICK 131

RESULT 21
Q8VIF6
ID Q8VIF6 PRELIMINARY; PRT; 742 AA.
AC Q8VIF6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Scavenger receptor with C-type lectin.
GN COLEC12 OR SRCL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21575692; PubMed=11718900;
RA Nakamura K., Funakoshi H., Tokunaga F., Nakamura T.;
RT "Molecular cloning of a mouse scavenger receptor with C-type lectin
RT (SRCL)(1), a novel member of the scavenger receptor family."
RT Biochim. Biophys. Acta 1522:53-58(2001).

DR EMBL; AB038519; BAB82497.1; -.
DR MGD; MGI:2152907; Colec12.
DR GO; GO:0006955; P:immune response; IDA.
DR GO; GO:0006910; P:phagocytosis, binding; IDA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF01391; Collagen; 2.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PRO0356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor; Lectin.
SQ SEQUENCE 742 AA; 81307 MW; 85A90D3AE881DB6B CRC64;

Query Match 14.5%; Score 159.5; DB 11; Length 742;
Best Local Similarity 33.1%; Pred. No. 1.2e-06;
Matches 49; Conservative 17; Mismatches 55; Indels 27; Gaps 8;

QY 17 CYKVIYFHDTSRRLNFEAEKACRRDGGQLVSISEDEQKLIKFIENLLPSDGFWIGL 76
Db 618 CY---YF--SLEKEILEDKLFCEDKSSHLVFINREEQQWIKKH---TVGRESHWIGL 668

QY 77 RRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP--SCGSEVCVVMYHQPSPAPAGIGGPY 135
Db 669 TDSEQESE-----WKWLDGSPVDYKXNWKAGQPDNMGSG-----HGPGEDCA-GLIY 713

QY 136 MFQWNDRCNMKNFICKYSDEKPAVPS 163
Db 714 AGQWPDFQCEINNFACE--KEREAVPS 739

RESULT 22
Q8CJ86
ID Q8CJ86 PRELIMINARY; PRT; 142 AA.
AC Q8CJ86;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SIGNR1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Skin;
RX MEDLINE=22133304; PubMed=12137941;
RA Parent S.A., Zhang T., Chretien G., Clemas J.A., Figueroa D.J., Ky B.,
RA Blevis R.A., Austin C.P., Rosen H.;
RT "Molecular characterization of the murine SIGNR1 gene encoding a C-
RT type lectin homologous to human DC-SIGN and DC-SIGNR."
RL Gene 293:33-46(2002).
DR EMBL; AF424802; AAN75597.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; LECTIN_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PRO0356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 142 AA; 16437 MW; 0CBB36A383D025EF CRC64;

Query Match 14.4%; Score 158; DB 11; Length 142;
Best Local Similarity 32.4%; Pred. No. 2.3e-07;
Matches 48; Conservative 21; Mismatches 45; Indels 34; Gaps 9;

QY 22 YFHDTSRRLNFEAEKACRRDGGQLVSISEDEQKLIKFIENLLPSDGFWIGLRRREE 81
Db 24 YFFSKSQR-NWMDAVTACKVEKVAQLVIINSDSEQ----TFLQOTSKAKGPTWGLSLDLKK 78


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DR      EMBL; AK007656; BAB25166.1; -
DR      HSP; P22897; 1EGG.
DR      MGD; MGI:1916415; Cd209b.
DR      GO; GO:0005529; F:sugar binding
DR      InterPro; IPR002353; Antifreeze
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; lectin_c; 1.
DR      PRINTS; PR00356; ANTIFREEZEII.
DR      SMART; SM00034; CLECT; 1.
DR      PROSITE; PS00615; C_TYPE_LLECTII
DR      PROSITE; PS50041; C_TYPE_LLECTII
DR      SEQUENCE 311 AA; 35618 MW;
SQ

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	Query Match	14.4%	Score 158;	DB 11;	Length 311;
	Best Local Similarity	32.4%;	Pred. NO. 5.8e-07;		
	Matches 48; Conservative	21;	Mismatches 45;	Indels 34;	Gaps 9;
Qy	22 YFHDTSRRLNFEAEKACRRDGGQLVSI ESEDEQKLIEKFIEIENLLPSDGDGFWIGLRRREE	81			
Dd	193 YFFSKSQ-R-NWNDAVTACKVEKAQLVIINSDEEQ----	TFLQQTSKAKGPTWMGLSLDKK	247		
Qy	82 QKSNSTACQDLYAWTDGSI--SQFRN-WYVDEP-SCGSEVCVVVMYHQPSAPAGIGGPYMF	137			
Dd	248 EAT-----WLWVDGSTLSRRFQKYWNRGEPNNIGEEDCVEF-----	AGDG-----	287		
Qy	138 QWNDDRCNMKNNFICKYSDEXPAVPSPRE	165			
Dd	288 -WNDSKCEKKFWICK-----KSATPCTE	310			

Search completed: September 9, 2004, 22:56:42
Job time : 73.3231 secs

Blank Sheet

Run on: September 9, 2004, 22:46:49 ; Search time 14.9631 Seconds
(without alignments)
706.418 Million cell updates/sec

Perfect score: 1100
Sequence: 1 RLLSGQPVCRGGTQPCYKV.....EEDAKKTFKESREAAINLAY 203

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 141681

Maximum DB seq length: 2000000000

Database : SwissProt 42:*

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	574	52.2		273	1	CHOD_MOUSE	Q9cxm0 mus musculus
2	561.5	51.0		273	1	CHOD_HUMAN	Q9h9p2 homo sapien
3	182	16.5		1456	1	MANR_HUMAN	P22897 homo sapien
4	177	16.1		1268	1	PGCN_MOUSE	P55066 mus musculus
5	176	16.0		1321	1	PGCN_HUMAN	O14594 homo sapien
6	174.5	15.9		3381	1	PGCV_BOVIN	P81282 bos taurus
7	174	15.8		1257	1	PGCN_RAT	P55067 rattus norv
8	174	15.8		2738	1	PGCV_RAT	Q9erb4 rattus norv
9	174	15.8		3358	1	PGCV_MOUSE	Q62059 mus musculus
10	174	15.8		3396	1	PGCV_HUMAN	P13611 homo sapien
11	171	15.5		3562	1	PGCV_CHICK	Q90953 gallus gall
12	164	14.9		643	1	CD93_RAT	Q9et61 rattus norv
13	158.5	14.4		2364	1	PGCA_BOVIN	P13608 bos taurus
14	158.5	14.4		2415	1	PGCA_HUMAN	P16112 homo sapien
15	155.5	14.1		2333	1	PGCA_CANFA	Q28343 canis famil
16	154.5	14.0		612	1	LEM2_MOUSE	Q00690 mus musculus
17	153.5	14.0		644	1	CD93_MOUSE	O89103 mus musculus
18	153.5	14.0		2124	1	PGCA_RAT	P07897 rattus norv
19	152	13.8		912	1	PGCB_BOVIN	Q28062 bos taurus
20	151.5	13.8		652	1	CD93_HUMAN	Q9npj3 homo sapien
21	151	13.7		197	1	CLE1_HUMAN	O75596 homo sapien
22	149	13.5		321	1	FCE2_HUMAN	P06734 homo sapien
23	147.5	13.4		2132	1	PGCA_MOUSE	Q61282 mus musculus
24	147	13.4		883	1	PGCB_MOUSE	Q61361 mus musculus
25	146	13.3		2109	1	PGCA_CHICK	P07898 gallus gall
26	145	13.2		158	1	LEC3_TRIST	Q9ygp1 trimeresuru
27	145	13.2		883	1	PGCB_RAT	P55068 rattus norv
28	144.5	13.1		173	1	LEC2_MEGRO	P17346 megabalanus
29	144.5	13.1		372	1	LEM1_RAT	P30836 rattus norv
30	143.5	13.0		372	1	LEM1_MOUSE	P18337 mus musculus
31	141.5	12.9		331	1	FCE2_MOUSE	P20693 mus musculus
32	141.5	12.9		549	1	LEM2_RAT	P98105 rattus norv
33	140.5	12.8		162	1	LEC3_MEGRO	P07439 megabalanus

DR SMART; SM00059; FN2; 1.
 DR SMART; SM00458; RICIN; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 6.
 DR PROSITE; PS0041; C_TYPE_LLECTIN_2; 8.
 DR PROSITE; PS00023; FIBRONECTIN_2; 1.
 DR PROSITE; PS00231; RICIN_B_LLECTIN; 1.
 KW Receptor; Signal; Calcium-binding; Transmembrane; Repeat;
 KW Glycoprotein; Endocytosis; Macrophage; Lectin; Antigen; 3D-structure.
 FT SIGNAL 1 18
 FT CHAIN 19 1456
 FT DOMAIN 19 1383
 FT TRANSMEM 1384 1411
 FT DOMAIN 1412 1456
 FT DOMAIN 22 142
 FT DOMAIN 157 212
 FT DOMAIN 216 344
 FT DOMAIN 360 490
 FT DOMAIN 502 629
 FT DOMAIN 644 781
 FT DOMAIN 805 926
 FT DOMAIN 943 1083
 FT DOMAIN 1100 1216
 FT DOMAIN 1228 1359
 FT DISULFID 646 659
 FT DISULFID 680 777
 FT DISULFID 753 769
 FT CARBOHYD 104 104
 FT CARBOHYD 344 344
 FT CARBOHYD 529 529
 FT CARBOHYD 926 926
 FT CARBOHYD 930 930
 FT CARBOHYD 1160 1160
 FT CARBOHYD 1205 1205
 FT CARBOHYD 1311 1311
 FT TURN 648 649
 FT STRAND 651 652
 FT TURN 654 655
 FT STRAND 658 663
 FT HELIX 667 669
 FT STRAND 671 671
 FT HELIX 673 683
 FT TURN 684 684
 FT STRAND 686 687
 FT HELIX 693 705
 FT TURN 706 707
 FT TURN 709 710
 FT STRAND 712 718
 FT TURN 723 724
 FT STRAND 727 727
 FT TURN 729 730
 FT STRAND 733 733
 FT TURN 741 742
 FT HELIX 746 748
 FT STRAND 752 757
 FT TURN 758 761
 FT STRAND 764 768
 FT TURN 769 770
 FT STRAND 773 780
 FT TURN 781 782
 SQ SEQUENCE 1456 AA; 166011 MW; 264E5AF3C576A5E3 CRC64;

Query Match 16.5%; Score 182; DB 1; Length 1456;
 Best Local Similarity 25.5%; Pred. No. 3.1e-08;
 Matches 52; Conservative 37; Mismatches 61; Indels 54; Gaps 8;
 QY 18 YKVIYFHTSRLNFEAEACRRDGGQLVSIQSEDEQKLEKFIENLLPSDGFWICLR 77
 Db 807 YKDYQYFSEKEKTMNARAFCKRNFGLVSIQSESEKFLWKYV-NRNDQAQAYFICLL 865
 QY 78 RREEKQSNSTACQDLYAWTDGSIQFRNMYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY 135
 Db 866 ISLDKK-----FAWMDGSKVDYVSWATGEPNFANEDENCVTMY-----SNSGF---- 908

QY 136 MFQWDDRCNMKNFICKYSDEK-----PAVPSREABGEETELTTPVLPEETQE----- 184
 Db 909 ---WINDINGCYPNAFICQHRHNSINATTVM-----TMPSVPSGCKEGWNFYSN 954
 QY 185 -----EDAKTKFKESREAAAL 199
 Db 955 KCFKIFGFMEERKNWQEARAKACI 978
 RESULT 4
 PGCN MOUSE
 ID_PGCN_MOUSE STANDARD; PRT; 1268 AA.
 AC P55066;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
 GN CSPG3 OR NCAN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=96039250; PubMed=7490074;
 RA Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.,
 RA Faessler R.;
 RT "Structure and chromosomal localization of the mouse neurocan gene.";
 RL Genomics 28:405-410(1995).
 CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
 development by binding to neural cell adhesion molecules (NG-CAM
 and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
 acid.
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 2 link domains.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X84727; CAA59216.1; -.
 DR PIR; S52781; S52781.
 DR HSSP; P00740; 1EDM.
 DR MGI; MGI:104694; Cspg3.
 DR InterPro; IPR002353; Antifreeze1.
 DR InterPro; IPR000152; Asx_hydroxyl_s.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR000538; Link.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00059; lectin_c; 1.
 DR Pfam; PF00084; sushi; 1.
 DR Pfam; PF00193; Xlink; 2.
 DR PRINTS; PR00356; ANTIFREEZE1.
 DR PRINTS; PR01265; LINKMODULE.
 DR ProDom; PD000918; Link; 2.
 DR SMART; SM00032; CCP; 1.

DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
KW EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 1268 NEUROCAN CORE PROTEIN.
FT DOMAIN 37 157 IG-LIKE V-TYPE.
FT DOMAIN 158 253 LINK 1.
FT DOMAIN 259 355 LINK 2.
FT DOMAIN 960 996 EGF-LIKE 1.
FT DOMAIN 998 1034 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1036 1165 C-TYPE LECTIN.
FT DOMAIN 1166 1224 SUSHI.
FT DISULFID 58 139 BY SIMILARITY.
FT DISULFID 181 252 BY SIMILARITY.
FT DISULFID 205 226 BY SIMILARITY.
FT DISULFID 279 354 BY SIMILARITY.
FT DISULFID 303 324 BY SIMILARITY.
FT DISULFID 964 975 BY SIMILARITY.
FT DISULFID 969 984 BY SIMILARITY.
FT DISULFID 986 995 BY SIMILARITY.
FT DISULFID 1040 1051 BY SIMILARITY.
FT DISULFID 1068 1160 BY SIMILARITY.
FT DISULFID 1136 1152 BY SIMILARITY.
FT DISULFID 1167 1210 BY SIMILARITY.
FT DISULFID 1196 1223 BY SIMILARITY.
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 742 742 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 978 978 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1175 1175 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1268 AA; 137200 MW; 3014E8E202A2FAEC CRC64;

Query Match 16.1%; Score 177; DB 1; Length 1268;
Best Local Similarity 31.5%; Pred. No. 7.5e-08;
Matches 45; Conservative 17; Mismatches 49; Indels 32; Gaps 6;

Qy 14 QPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSIESEDEQKLEKFIENLLPSDGF 73
Db 1048 QGHCYR--YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW 1096
Qy 74 IGLRRREKQSNSTACQDIYAWTDGSIQFRNWWYDEPS---CGSEVCVVMYHQPAPAG 130
Db 1097 IGLNDRTVRD-----FQWIDNTGLQYENWREKQPDNFFAGGEDCVVMVAHESG--- 1145
Qy 131 IGGPYMFQWDDRCNMKNFICK 153
Db 1146 -----RWNDVPCNYNLPYVCK 1161

RESULT 5
PGCN HUMAN STANDARD; PRT; 1321 AA.
AC O14594; Q9UPK6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
GN CSPG3 OR NCAN OR NEUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
[1] SEQUENCE FROM N.A.
RX MEDLINE=99013874; PubMed=9795216;
RA Prange C.K., Pennacchio L.A., Lieuallen K., Fan W., Lennon G.G.;
RT "Characterization of the human neurocan gene, CSPG3.";
RL Gene 221:199-205(1998).
[2] SEQUENCE OF 1-990 AND 1007-1321 FROM N.A., AND VARIANT ALA-1254.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of an ~1 Mb region containing the MEF2B gene in
19p12.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: May modulate neuronal adhesion and neurite growth during
development by binding to neural cell adhesion molecules (NG-CAM
and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
acid.
CC !- TISSUE SPECIFICITY: Brain.
CC !- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC !- SIMILARITY: Contains 2 EGF-like domains.
CC !- SIMILARITY: Contains 2 link domains.
CC !- SIMILARITY: Contains 1 C-type lectin family domain.
CC !- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC !- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
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CC -----
CC EMBL; AF026547; AAC80576.1; -.
CC EMBL; AC003110; AAB86655.1; -.
CC EMBL; AC005254; AAC25581.1; -.
CC HSSP; P00740; 1EDM.
CC Genew; HGNC:2465; CSPG3.
CC MIM; 600826; -.
CC InterPro; IPR000152; Asx_hydroxyl_s.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR007110; IG_Like.
CC InterPro; IPR003599; IG.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00047; ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 2.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 2.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00445; LINK; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 3.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS00026; EGF_3; 2.

DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
KW EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal; Polymorphism.
FT SIGNAL 1 22
FT CHAIN 23 1321 NEURON CORE PROTEIN.
FT DOMAIN 38 153 IG-LIKE V-TYPE.
FT DOMAIN 159 254 LINK 1.
FT DOMAIN 260 356 LINK 2.
FT DOMAIN 1008 1044 EGF-LIKE 1.
FT DOMAIN 1046 1082 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1084 1213 C-TYPE LECTIN.
FT DOMAIN 1214 1272 SUSHI.
FT DISULFID 59 140 BY SIMILARITY.
FT DISULFID 182 253 BY SIMILARITY.
FT DISULFID 206 227 BY SIMILARITY.
FT DISULFID 280 355 BY SIMILARITY.
FT DISULFID 304 325 BY SIMILARITY.
FT DISULFID 1012 1023 BY SIMILARITY.
FT DISULFID 1017 1032 BY SIMILARITY.
FT DISULFID 1034 1043 BY SIMILARITY.
FT DISULFID 1088 1099 BY SIMILARITY.
FT DISULFID 1116 1208 BY SIMILARITY.
FT DISULFID 1184 1200 BY SIMILARITY.
FT DISULFID 1215 1258 BY SIMILARITY.
FT DISULFID 1244 1271 BY SIMILARITY.
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1026 1026 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1223 1223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 1254 1254 V -> A (in dbSNP:1064389).
FT CONFLICT 1234 1234 N -> Y (IN REF. 2).
FT CONFLICT 1282 1282 G -> R (IN REF. 2).
SQ SEQUENCE 1321 AA; 142972 MW; 2EF47F823DB980B8 CRC64;

Query Match 16.0%; Score 176; DB 1; Length 1321;
Best Local Similarity 31.5%; Pred. No. 9.6e-08;
Matches 45; Conservative 18; Mismatches 48; Indels 32; Gaps 6;

QY 14 QRPCYKVIYFHTSRRLNFEAEKACRRDGGQLVSIIESEDEQKLEKFIENLLPSDGF 73
Db 1096 QGHCYR--YF---AHRRAWEDAEDKDCRRRSHGLTSVHSPEHSFNSF-----GHENTW 1144

QY 74 IGLRREKQSNSTACQDLYAWTDGSGISQFNWYVDEPS---CGSEVCVMYHQPSAPAG 130
Db 1145 IGLNDRIVERD-----FQWTDNTGLQFNWRENQPDNFFAGGEDCVMVAHESG--- 1193

QY 131 IGGPYMFQWDDRCNMKNFICK 153
Db 1194 -----RWNDVPCNPNLPYVCK 1209

RESULT 6
PGCV_BOVIN STANDARD; PRT; 3381 AA.
AC P81282; O77609; O77610; O77611; O77612;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Versican core protein precursor (Large fibroblast proteoglycan)
DE Chondroitin sulfate proteoglycan core protein 2 (PG-M) (Glial
DE hyaluronate-binding protein) (GHAP).
GN CP5G2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS VO; V1; V2 AND V3).
RC TISSUE=Forebrain;

RX MEDLINE=98288320; PubMed=9624174;
RA Schmalfeldt M.; Dours-Zimmermann M.T.; Winterhalter K.H.;
RA Zimmermann D.R.;
RT "Versican V2 is a major extracellular matrix component of the mature
RT bovine brain.";
RL J. Biol. Chem. 273:15758-15764(1998).
RN [2]
RP SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
RP AND 342-348.
RC TISSUE=Spinal cord;
RX MEDLINE=92062692; PubMed=1720020;
RA Perides G.; Biviano F.; Bignami A.;
RT "Interaction of a brain extracellular matrix protein with hyaluronic
RT acid.";
RL Biochim. Biophys. Acta 1075:248-258(1991).
CC -!- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -!- SUBUNIT: Interacts with FBLN1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=P81282-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=P81282-2; Sequence=VSP_003078, VSP_003079;
CC Name=V2;
CC IsoId=P81282-3; Sequence=VSP_003080;
CC Name=V3;
CC IsoId=P81282-4; Sequence=VSP_003078, VSP_003081;
CC TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 are expressed
CC in the central nervous system, and in a number of mesenchymal and
CC epithelial tissues; the major isoform V2 is restricted to the
CC central nervous system.
CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
CC (By similarity).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC
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CC
CC EMBL; AF060456; AAC24358.1; -.
CC EMBL; AF060457; AAC24359.1; -.
CC EMBL; AF060458; AAC24360.1; -.
CC EMBL; AF060459; AAC24361.1; -.
CC PIR; T14274; T14274.
CC PIR; T42389; T42389.
CC HSSP; P01132; 1EPG.
CC InterPro; IPR000152; Asx hydroxyl_s.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR007110; Ig-Like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00047; ig; 1.
CC Pfam; PF00059; lectin_C; 1.
CC Pfam; PF00084; sushi; 1.

DR pfam; PF00193; Xlink; 2.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 3381
FT DOMAIN 21 147
FT DOMAIN 168 245
FT DOMAIN 266 347
FT DOMAIN 349 1336
FT DOMAIN 1337 3074
FT DOMAIN 3074 3110
FT DOMAIN 3112 3148
FT DOMAIN 3161 3275
FT DOMAIN 3280 3338
FT DISULFID 44 131
FT DISULFID 173 244
FT DISULFID 197 218
FT DISULFID 271 346
FT DISULFID 295 316
FT DISULFID 3078 3089
FT DISULFID 3083 3098
FT DISULFID 3100 3109
FT DISULFID 3116 3127
FT DISULFID 3121 3136
FT DISULFID 3138 3147
FT DISULFID 3154 3165
FT DISULFID 3182 3274
FT DISULFID 3250 3266
FT DISULFID 3281 3324
FT DISULFID 3310 3337
FT CARBOHYD 57 57
FT CARBOHYD 331 331
FT CARBOHYD 352 352
FT CARBOHYD 817 817
FT CARBOHYD 965 965
FT CARBOHYD 1017 1017
FT CARBOHYD 1333 1333
FT CARBOHYD 1393 1393
FT CARBOHYD 1437 1437
FT CARBOHYD 1463 1463
FT CARBOHYD 1653 1653
FT CARBOHYD 1974 1974
FT CARBOHYD 2045 2045
FT CARBOHYD 2074 2074
FT CARBOHYD 2103 2103
FT CARBOHYD 2263 2263
FT CARBOHYD 2290 2290
FT CARBOHYD 2356 2356
FT CARBOHYD 2623 2623
FT CARBOHYD 2641 2641
FT CARBOHYD 2919 2919
FT CARBOHYD 3052 3052
FT CARBOHYD 3354 3354
FT CARBOHYD 3364 3364
FT VARSPLIC 349 349
P -> R (in isoform V1 and isoform V3).

FT VARSPLIC 350 1336 /FTid=VSP_003078.
FT Missing (in isoform V1).
FT /FTid=VSP_003079.
FT Missing (in isoform V2).
FT /FTid=VSP_003080.
FT Missing (in isoform V3).
FT /FTid=VSP_003081.
FT MISSING (IN REF. 2).
FT MISSING (IN REF. 2).
FT N -> D (IN REF. 2).
FT Q -> D (IN REF. 2).
FT CONFLICT 346 346 C -> R (IN REF. 2).
SQ SEQUENCE 3381 AA; 369984 MW; F09716FA7778D459 CRC64;
Query Match 15.9%; Score 174.5; DB 1; Length 3381;
Best Local Similarity 25.5%; Pred. No. 4.2e-07;
Matches 59; Conservative 26; Mismatches 71; Indels 75; Gaps 11;
QY 14 QRPCYKVIYFHDTSRRLNFEFAKEACRRDGGQLVSISEDEQKLIKFIENLLPSDGF- 72
Db 3162 QGCYK--YF---AHRRTWDAARECRLOGAHLTSILSHEEQMFVNRV-----GHDYQ 3209
QY 73 WIGLRREEKQSNSTACQDIYAWTDGSIQFRNYYVDEP---SCGEVCVVMYHQSAP 128
Db 3210 WIGL-----NDKMFEDHFRWTDGSTLQYENWRPNQDSFFSTGEDCVVIWHENG-- 3259
QY 129 AGIGPYMFQWNDRCNMKNFICKYS---DEKPAVPSREAEGE----- 169
Db 3260 -----QWNDVPCNVHLTYTCKKGTVACGQPPVVENAKTFGKMKPRYEINSLRYHC 3310
QY 170 -----ETELTT-----PVL-----PEETQEEDAKKTFKESREAAALN 200
Db 3311 KDGFIQRHLPTIRCLNGRWAMPKITCLNPSAYQRTYSKKYFKNSSSAKDN 3361
RESULT 7
PGCN RAT STANDARD; PRT; 1257 AA.
ID_PGCN RAT
AC P55067;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
DE (245 kDa early postnatal core glycoprotein) [Contains: 150 kDa adult
DE core glycoprotein].
GN CSPG3 OR NCAN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=92406907; PubMed=1326557;
RA Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
RT "Cloning and primary structure of neurocan, a developmentally
RT regulated, aggregating chondroitin sulfate proteoglycan of brain.";
RL J. Biol. Chem. 267:19536-19547(1992).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=94230574; PubMed=7513709;
RA Friedlander D.R., Milev P., Karthikeyan L., Margolis R.K.,
RA Margolis R.U., Grumet M.;
RT "The neuronal chondroitin sulfate proteoglycan neurocan binds to the
RT neural cell adhesion molecules Ng-CAM/L1/NILE and N-CAM, and inhibits
RT neuronal adhesion and neurite outgrowth.";
RL J. Cell Biol. 125:669-680(1994).
CC -!- FUNCTION: May modulate neuronal adhesion and neurite growth during
CC development by binding to neural cell adhesion molecules (NG-CAM
CC and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
CC acid.
CC -!- TISSUE SPECIFICITY: Early postnatal and adult brain; not expressed
CC in kidney, lung, liver and muscle.

CC -!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND
CC O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
CC -!- PTM: TWO ISOFORMS WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC
CC DEGRADATION. THE LARGE ISOFORM IS PREDOMINANT IN EARLY POSTNATAL
CC BRAIN, THE SMALL ISOFORM IS FOUND IN ADULT BRAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 LINK DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE AGGREGAN/VERSICAN PROTEOGLYCAN FAMILY.
CC -----
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CC -----
CC EMBL; M97161; AAC37679.1; -.
CC PIR; S28764; S28764.
CC HSSP; P00740; IEDM.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR000152; Asx_hydroxyl_s.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR007110; Ig_Like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00059; lectin_C; 1.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 2.
CC PRINTS; PR00356; ANTIFREEZEII.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 2.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00409; IG_1.
CC SMART; SM00445; LINK; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00615; C-TYPE LECTIN_1; 1.
CC PROSITE; PS00041; C-TYPE LECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 3.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS00026; EGF_3; 2.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00835; IG_Like; 1.
CC PROSITE; PS01241; LINK; 2.
CC Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
KW EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
FT SIGNAL 1 22
FT CHAIN 23 1257 NEUROCAN CORE PROTEIN.
FT CHAIN 639 1257 150 kDa ADULT CORE GLYCOPROTEIN.
FT DOMAIN 37 157 IG-LIKE V-TYPE.
FT DOMAIN 158 253 LINK 1.
FT DOMAIN 259 355 LINK 2.
FT DOMAIN 949 985 EGF-LIKE 1.
FT DOMAIN 987 1023 EGF-LIKE 2.
FT DOMAIN 1025 1154 C-TYPE LECTIN.
FT DOMAIN 1155 1213 SUSHI.
FT DISULFID 58 139 BY SIMILARITY.
FT DISULFID 181 252 BY SIMILARITY.
FT DISULFID 205 226 BY SIMILARITY.
FT DISULFID 279 354 BY SIMILARITY.
FT DISULFID 303 324 BY SIMILARITY.
FT DISULFID 953 964 BY SIMILARITY.

FT DISULFID 958 973 BY SIMILARITY.
FT DISULFID 975 984 BY SIMILARITY.
FT DISULFID 1029 1040 BY SIMILARITY.
FT DISULFID 1057 1149 BY SIMILARITY.
FT DISULFID 1125 1141 BY SIMILARITY.
FT DISULFID 1156 1199 BY SIMILARITY.
FT DISULFID 1185 1212 BY SIMILARITY.
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 737 737 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 944 944 O-LINKED (XYL. . .) (CHONDROITIN SULFATE).
FT CARBOHYD 967 967 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1164 1164 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1257 AA; 135544 MW; 992B33DCFA19EE1B CRC64;
Query Match 15.8%; Score 174; DB 1; Length 1257;
Best Local Similarity 30.8%; Pred.No. 1.4e-07;
Matches 44; Conservative 18; Mismatches 49; Indels 32; Gaps 6;
QY 14 QRPCYKVIYFHDTSRLNFEAKEACRRDGGQGLVLSIESEDEQKLIKFIENLLPSDGF 73
Db 1037 QGHCYR--YF--AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW 1085
QY 74 IGLRRREKQSNSTACQDLYAWTDCSISQFRNWNVDPS---CGSEVCVMYHQPSAPAG 130
Db 1086 IGLNDRTVERD-----FQWTDNTCLQYENWREKQPDNFFAGGEDCVVMVAHENG--- 1134
QY 131 IGGPYMFQWMDRCNMKNFICK 153
Db 1135 -----RWNDVPCNPNLPYVCK 1150
RESULT 8
PGCV_RAT STANDARD; PRT; 2738 AA.
AC Q9ERB4; O08592; O88564; Q9R1K4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Versican core protein precursor (Large fibroblast proteoglycan)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
DE hyaluronate-binding protein) (GHAP) (Fragments).
GN CPBG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 349-2738 FROM N.A. (ISOFORM V0), SEQUENCE FROM N.A.
RP (ISOFORM V3), AND SEQUENCE OF 2657-2738 FROM N.A. (ISOFORM VINT).
RC STRAIN=Wistar Kyoto;
RX MEDLINE=99327053; PubMed=10397680;
RA Lemire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,
RA Wight T.N.;
RT "Versican/PG-M isoforms in vascular smooth muscle cells";
RL Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
RN [2]
RP SEQUENCE OF 349-2738 FROM N.A. (ISOFORM V0).
RC STRAIN=Wistar Kyoto;
RX MEDLINE=98308094; PubMed=9642104;
RA Milev P., Maurel P., Chiba A., Mevissen M., Popp S., Yamaguchi Y.,
RA Margolis R.K., Margolis R.U.;
RT "Differential regulation of expression of hyaluronan-binding
RT proteoglycans in developing brain: aggrecan, versican, neurocan, and
RT brevican";
RL Biochem. Biophys. Res. Commun. 247:207-212(1998).
RN [3]
RP SEQUENCE OF 2421-2463 FROM N.A. (ISOFORM V0).
RC TISSUE=Kidney;
RX MEDLINE=98094159; PubMed=9434070;
RA Pyke C., Kristensen P., Ostergaard P.B., Oturai P.S., Romer J.;
RT "Proteoglycan expression in the normal rat kidney";
RL Nephron 77:461-470(1997).


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RESULT 9
PGCV_MOUSE STANDARD; PRT; 3358 AA.
AC PGCV_MOUSE Q62058; Q9CUU0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Versican core protein precursor (Large fibroblast proteoglycan)
DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).
GN CSPG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS V0; V1 AND V2).
RC STRAIN=C57BL/6; and Swiss Webster; TISSUE=Brain;
RX MEDLINE=95122551; PubMed=7822336;
RA Ito K., Shinomura T., Zako M., Ujita M., Kimata K.;
RT "Multiple forms of mouse PG-M, a large chondroitin sulfate
RT proteoglycan generated by alternative splicing.";
RL J. Biol. Chem. 270:958-965(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM V3).
RC STRAIN=C57BL/6;
RX MEDLINE=95181355; PubMed=7876137;
RA Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
RT "Expression of PG-M(V3), an alternatively spliced form of PG-M
RT without a chondroitin sulfate attachment in region in mouse and human
RT tissues.";
RL J. Biol. Chem. 270:3914-3918(1995).
RN [3]
RP SEQUENCE OF 1-1692 FROM N.A. (ISOFORM V1).
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP INTERACTION WITH FBLN1.
RX MEDLINE=99329059; PubMed=10400671;
RA Asperger A., Adam S., Kostka G., Timpl R., Heinegaard D.;
RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
RT versican.";
RL J. Biol. Chem. 274:20444-20449(1999).
CC -!- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
```

```
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=Q62059-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=Q62059-2; Sequence=VSP_003087, VSP_003088;
CC Name=V2;
CC IsoId=Q62059-3; Sequence=VSP_003089;
CC Name=V3;
CC IsoId=Q62059-4; Sequence=VSP_003087, VSP_003090;
CC -!- TISSUE SPECIFICITY: V2 is found only in brain.
CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC
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CC
CC EMBL; D16263; BAA03796.1; -.
CC EMBL; D28599; -; NOT ANNOTATED_CDS.
CC EMBL; D32040; BAA06802.1; -.
CC EMBL; AK014525; BAB29411.2; -.
CC HSSP; P01132; IEPG.
CC MGD; MGI:102889; Cspg2.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR007110; Ig_like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 2.
CC PRINTS; PR01265; LINKMODULE.
CC PRODOM; PD000918; Link; 2.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00445; LINK; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1_2.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS00026; EGF_3; 2.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS01241; LINK; 2.
CC Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
CC Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
CC Hyaluronic acid; Alternative splicing.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 3358 VERSICAN CORE PROTEIN.
FT
```

FT	DOMAIN	21	146	IG-LIKE V-TYPE.	
FT	DOMAIN	167	244	LINK 1.	
FT	DOMAIN	265	346	LINK 2.	
FT	DOMAIN	348	1308	GAG-ALPHA (GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN).	
FT	DOMAIN	1309	3052	GAG-BETA.	
FT	DOMAIN	3052	3088	EGF-LIKE 1.	
FT	DOMAIN	3090	3126	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).	
FT	DOMAIN	3139	3253	C-TYPE LECTIN.	
FT	DOMAIN	3258	3316	SUSHI.	
FT	DISULFID	44	130	BY SIMILARITY.	
FT	DISULFID	172	243	BY SIMILARITY.	
FT	DISULFID	196	217	BY SIMILARITY.	
FT	DISULFID	270	333	BY SIMILARITY.	
FT	DISULFID	294	315	BY SIMILARITY.	
FT	DISULFID	3056	3067	BY SIMILARITY.	
FT	DISULFID	3061	3076	BY SIMILARITY.	
FT	DISULFID	3078	3087	BY SIMILARITY.	
FT	DISULFID	3094	3105	BY SIMILARITY.	
FT	DISULFID	3099	3114	BY SIMILARITY.	
FT	DISULFID	3116	3125	BY SIMILARITY.	
FT	DISULFID	3132	3143	BY SIMILARITY.	
FT	DISULFID	3160	3252	BY SIMILARITY.	
FT	DISULFID	3228	3244	BY SIMILARITY.	
FT	DISULFID	3259	3302	BY SIMILARITY.	
FT	DISULFID	3288	3315	BY SIMILARITY.	
FT	CARBOHYD	57	57	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	330	330	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	351	351	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	441	441	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	807	807	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	914	914	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	951	951	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	1305	1305	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	1372	1372	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	1679	1679	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	2054	2054	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	2244	2244	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	2362	2362	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	2627	2627	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	3030	3030	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	3332	3332	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYD	3342	3342	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	VARSPPLIC	348	348	P -> R (in isoform V1 and isoform V3).	
FT				/FTid=VSP 003087.	
FT	VARSPPLIC	349	1308	Missing (in isoform V1).	
FT				/FTid=VSP 003088.	
FT	VARSPPLIC	1309	3052	Missing (in isoform V2).	
FT				/FTid=VSP 003089.	
FT	VARSPPLIC	349	3052	Missing (in isoform V3).	
FT				/FTid=VSP 003090.	
FT	CONFLICT	126	126	A -> G (IN REF. 3).	
FT	CONFLICT	348	348	MISSING (IN REF. 3).	
FT	CONFLICT	1658	1658	I -> T (IN REF. 3).	
FT	CONFLICT	1674	1680	TVWNSNS -> QFGIQT (IN REF. 3).	
SQ	SEQUENCE	3358 AA;	366938 MW;	071B80026BC0762D CRC64;	
Query Match					15.8%; Score 174; DB 1; Length 3358;
Best Local Similarity					28.5%; Pred. No. 4.6e-07;
Matches					47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
Qy	14	QRPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIQFRNYYVDEP----	SCGSEVCVVMYHQPSAP 128		
Db	3140	QGQCYK--YF---AHRRTWDAERECLQGAHLTSILSHEEQMFVNRV-----	GHDYQ 3187		
Qy	73	WIGLRRREKQSNSTACQDLYAWTDGSIQFRNYYVDEP----	SCGSEVCVVMYHQPSAP 128		
Db	3188	WIGL-----NDKMFEDHDFRTDGSALQYENWRPNQDSFFSAGEDCVVIWHENG--	3237		
Qy	129	AGIGGPFYMFQWDDRCNMKNFKCKYS-----DEKPAVPSREAEGE 169			
Db	3238	-----QWNDVPCNYHLTYTCKKGTACGQPPVVENAKTEGK 3273			

PGCV_HUMAN	STANDARD;	PRT;	3396 AA.
ID	PI3611; P20754; Q13010; Q13189; Q15123; Q9UNW5;		
AC	01-JAN-1990 (Rel. 13, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Versican core protein precursor (Large fibroblast proteoglycan)		
DE	(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial hyaluronate-binding protein) (GHAP).		
DE	CSPG2.		
GN	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID=9606;		
OX	[1]		
RN	SEQUENCE FROM N.A. (ISOFORM V0).		
RP	MEDLINE=95105188; PubMed=7528742;		
RX	Naso M.F., Zimmermann D.R., Iozzo R.V.;		
RA	"Characterization of the complete genomic structure of the human versican gene and functional analysis of its promoter.";		
RT	J. Biol. Chem. 269:32999-33008(1994).		
RL	[2]		
RN	SEQUENCE FROM N.A. (ISOFORM V1).		
RP	TISSUE=Placenta;		
RC	MEDLINE=90059882; PubMed=2583089;		
RX	Zimmermann D.R., Ruoslahti E.;		
RA	"Multiple domains of the large fibroblast proteoglycan, versican.";		
RT	EMBO J. 8:2975-2981(1989).		
RL	[3]		
RN	SEQUENCE FROM N.A. (ISOFORM V2).		
RP	TISSUE=Glial tumor;		
RC	MEDLINE=95105187; PubMed=7806529;		
RX	Dours-Zimmermann M.T., Zimmermann D.R.;		
RA	"A novel glycosaminoglycan attachment domain identified in two alternative splice variants of human versican.";		
RT	J. Biol. Chem. 269:32992-32998(1994).		
RL	[4]		
RN	SEQUENCE OF 2711-3396 FROM N.A.		
RP	TISSUE=Lung fibroblast;		
RC	MEDLINE=88007514; PubMed=2820964;		
RX	Krusius T., Gehlsen K.R., Ruoslahti E.;		
RA	"A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like and growth factor-like sequences.";		
RT	J. Biol. Chem. 262:13120-13125(1987).		
RL	[5]		
RN	SEQUENCE OF 251-347 FROM N.A.		
RP	MEDLINE=9312792; PubMed=1478664;		
RX	Iozzo R.V., Naso M.F., Cannizzaro L.A., Wasmuth J.J.;		
RA	McPherson J.D.;		
RT	"Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chromosome 5 (5q12-5q14).";		
RL	Genomics 14:845-851(1992).		
RN	[6]		
RP	SEQUENCE FROM N.A. (ISOFORM V3).		
RC	TISSUE=Brain;		
RX	MEDLINE=95181355; PubMed=7876137;		
RA	Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;		
RT	"Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and human tissues.";		
RL	J. Biol. Chem. 270:3914-3918(1995).		
RN	[7]		
RP	SEQUENCE OF 3333-3396 FROM N.A. (ISOFORM VINT).		
RC	TISSUE=Aortic smooth muscle;		
RX	MEDLINE=99327053; PubMed=10397680;		
RA	LeMire J.M., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.;		
RT	"Versican/PG-M isoforms in vascular smooth muscle cells.";		
RL	Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).		
RN	[8]		
RP	PARTIAL SEQUENCE.		

```
RC TISSUE=Brain;
RX MEDLINE=89174663; PubMed=2466833;
RA Perides G., Lane W.S.; Andrews D., Dahl D., Bignami A.;
RT "Isolation and partial characterization of a glial
RT hyaluronate-binding protein.";
RL J. Biol. Chem. 264:5981-5987(1989).
RN [9]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX MEDLINE=96213482; PubMed=8627343;
RA Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;
RT "Differential expression of versican isoforms in brain tumors.";
RL J. Neuropathol. Exp. Neurol. 55:528-533(1996).
CC -!- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -!- SUBUNIT: Interacts with FBLN1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=P13611-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=P13611-2; Sequence=VSP_003082, VSP_003083;
CC Name=V2;
CC IsoId=P13611-3; Sequence=VSP_003084;
CC Name=V3;
CC IsoId=P13611-4; Sequence=VSP_003082, VSP_003085;
CC Name=Vint;
CC IsoId=P13611-5; Sequence=VSP_003086;
CC -!- TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed
CC in normal brain, gliomas, medulloblastomas, schwannomas,
CC neurofibromas, and meningiomas; v2 is restricted to normal brain
CC and gliomas; v3 is found in all these tissues except
CC medulloblastomas.
CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
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CC -----
DR EMBL; U16306; AAG5018.1; -.
DR EMBL; X15998; CAA34128.1; -.
DR EMBL; S52488; AAB24878.1; -.
DR EMBL; U26555; AAA67565.1; -.
DR EMBL; D32039; BAA06801.1; -.
DR EMBL; J02814; AAA36437.1; -.
DR EMBL; AF084545; AAD48545.1; -.
DR PIR; S06014; A60979.
DR HSSP; P01132; 1EGF.
DR Genew; HGNC:2454; CSPG2.
DR MIM; 118661; -.
DR GO; GO:0005578; C:extracellular matrix; TAS.
DR GO; GO:0005540; F:hyaluronic acid binding; TAS.
DR GO; GO:0008037; P:cell recognition; TAS.
DR GO; GO:0007275; P:development; TAS.
DR InterPro; IPR000152; Asx_hydroxyl_s.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003599; Ig.

DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; Xlink; 2.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1_2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
KW Hyaluronic acid; Alternative splicing.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 3396 VERSICAN CORE PROTEIN.
FT DOMAIN 21 146 IG-LIKE V-TYPE.
FT DOMAIN 167 244 LINK 1.
FT DOMAIN 265 346 LINK 2.
FT DOMAIN 348 1335 GAG-ALPHA
(GLYCOSAMINOGLYCAN ATTACHMENT DOMAIN).
FT DOMAIN 1336 3089 GAG-BETA.
FT DOMAIN 3089 3125 EGF-LIKE 1.
FT DOMAIN 3127 3163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3176 3290 C-TYPE LECTIN.
FT DOMAIN 3295 3353 SUSHI.
FT DISULFID 44 130 BY SIMILARITY.
FT DISULFID 172 243 BY SIMILARITY.
FT DISULFID 196 217 BY SIMILARITY.
FT DISULFID 270 345 BY SIMILARITY.
FT DISULFID 294 315 BY SIMILARITY.
FT DISULFID 3093 3104 BY SIMILARITY.
FT DISULFID 3098 3113 BY SIMILARITY.
FT DISULFID 3115 3124 BY SIMILARITY.
FT DISULFID 3131 3142 BY SIMILARITY.
FT DISULFID 3136 3151 BY SIMILARITY.
FT DISULFID 3153 3162 BY SIMILARITY.
FT DISULFID 3169 3180 BY SIMILARITY.
FT DISULFID 3197 3289 BY SIMILARITY.
FT DISULFID 3265 3281 BY SIMILARITY.
FT DISULFID 3296 3339 BY SIMILARITY.
FT DISULFID 3325 3352 BY SIMILARITY.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 15.8%; Score 174; DB 1; Length 3396;
Best Local Similarity 28.5%; Pred. No. 4.7e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;

QY 14 ORPCYKVIYFHDTSRRRLNFEFAKEACRRDGGQLVLSIESEDEQKLEKFIENLLESDGDF- 72
Db 3177 QGQCYK--YF---AHRRTWDAARECRLOGAHLTSILSHEEQMFVNRV-----GHDIYQ 3224

QY 73 WIGLRREKQSNSTACQDLYAWTDGSIQFRNYYVDEP----SCGSEVCVMYHQPSAP 128
Db 3225 WIGL-----NDKMFEDHDFWTDGSTLOQENWRPNQDSFFSAGEDCVVIWHENG-- 3274

QY 129 AGIGGPFYMFQWDDRCNKKNFICKYS----DEKPAVPSREAGE 169
Db 3275 -----QWNDVPCNYHLTYTCKKGTACGQPPVVENAKTFGK 3310
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Query Match      15.5%; Score 171; DB 1; Length 3562;
Best Local Similarity 28.5%; Pred. No. 9.2e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;

QY 14 QRCYKVIYFHDTSRRRLNFEAEACRRDGGQLVSISEDEQKLEKFIENLLPSDGF- 72
Db 3342 QGQYK--YF---AHRRTWDTARECRLOGAHLTSLSHSEEQVFNRI-----GHDYQ 3389

QY 73 WIGLRREEKQSNSTACQDLYAWTDGSIQFRNWNVDPEP---SCGSEVCVVMYHQPSAP 128
Db 3390 WIGL-----NDKMFERDFRWTGDSPLQYENWRPNQDPSFFSAGEDCVVLIWHENG-- 3439

QY 129 AGIGGPFYFQWDDRCNMKNFICKYS-----DEKPAVPSRAEGE 169
Db 3440 -----QWNVPCNYHLTYTCKKGTVACGQPPVVENAKTFGK 3475

RESULT 12
CD93_RAT
ID CD93_RAT STANDARD; PRT; 643 AA.
AC Q9ET61; Q9J126;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Complement component C1q receptor precursor (Complement component 1, q
DE subcomponent, receptor 1) (ClqR) (ClqR(p)) (Clq/MBL/SPA receptor)
DE (CD93 antigen) (Cell surface antigen AA4).
GN C1QR1 OR CD93 OR C1QRP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PVG; TISSUE=Natural killer cells;
RX MEDLINE=20545218; PubMed=11093152;
RA Lovik G., Vaage J.T., Dissen E., Szpirer C., Ryan J.C., Rolstad B.;
RT "Characterization and molecular cloning of rat ClqR, a receptor on NK
RT cells.";
RL Eur. J. Immunol. 30:3355-3362(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Lung;
RX MEDLINE=20507883; PubMed=10934210;
RA Dean Y.D., McGreal E.P., Akatsu H., Gasque P.;
RT "Molecular and cellular properties of the rat AA4 antigen, a C-type
RT lectin-like receptor with structural homology to thrombomodulin.";
RL J. Biol. Chem. 275:34382-34392(2000).
CC -!- FUNCTION: Receptor (or element of a larger receptor complex) for
CC C1q, mannose-binding lectin (MBL2) and pulmonary surfactant
CC protein A (SPA). May mediate the enhancement of phagocytosis in
CC monocytes and macrophages upon interaction with soluble defense
CC collagens. May play a role in intercellular adhesion.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed. Highly expressed in lung and
CC heart. Expressed at lower level in brain, thymus, liver, spleen,
CC intestine, kidney, adrenal gland, muscle and testis. Expressed on
CC endothelial cells, platelets, undifferentiated monocytes and
CC circulating natural killer cells.
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 5 EGF-like domains.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF136537; AAG01572.1; -
CC EMBL; AF160978; AAF80402.1; -
DR
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DR HSSP; P35555; IEMN.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0004872; F:receptor activity; ISS.
DR GO; GO:0016337; P:cell-cell adhesion; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.
DR GO; GO:0006909; P:phagocytosis; ISS.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 3.
KW Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
KW EGF-like domain; Lectin; Glycoprotein.
FT SIGNAL 1 23
FT CHAIN 24 643
FT DOMAIN 24 571
FT TRANSMEM 572 592
FT DOMAIN 593 643
FT DOMAIN 31 173
FT DOMAIN 257 298
FT DOMAIN 299 341
FT DOMAIN 342 381
FT DOMAIN 382 423
FT DOMAIN 424 462
FT DISULFID 261 272
FT DISULFID 268 282
FT DISULFID 284 297
FT DISULFID 303 314
FT DISULFID 308 325
FT DISULFID 327 340
FT DISULFID 346 355
FT DISULFID 351 364
FT DISULFID 366 380
FT DISULFID 386 397
FT DISULFID 393 406
FT DISULFID 408 422
FT DISULFID 428 437
FT DISULFID 433 446
FT DISULFID 448 461
FT CARBOHYD 322 322
FT CARBOHYD 498 498
FT CONFLICT 417 417
SQ SEQUENCE 643 AA; 68781 MW; 9AE4C933AD943DB6 CRC64;

Query Match      14.9%; Score 164; DB 1; Length 643;
Best Local Similarity 25.5%; Pred. No. 4.7e-07;
Matches 49; Conservative 33; Mismatches 70; Indels 40; Gaps 9;

QY 8 VCRGGTQRCYKVIYFHDTSRRRLNFEAEACRRDGGQLVSISEDEQKLEKFIENLL- 66
Db 29 VCEG---TACYTAHW-----GKLISAAEAQHRCNENGNNLATVKSEEEARHVQEAQLLK 80

QY 67 ---PSD---GDFWIGLRREEKQSNSTACQDLYAWT-DGSIQFRNWNV-VDEPSCGSEVC 118
Db 81 TKAPSETKIGKFWIGLQREKGRCTYHDLPMKGFWSVGGEDTYSNWKASKSKSKRC 140

QY 119 VVMY-----HQPAPAGIGGPFYMFQWNNDRD-----NMKNFICKYSDEKPAVPSR 164
Db 141 VSLILDLSLKPSPHLP-----KWHESPCGTPDAPGNSIEGFLCKFNFKMGCSPLA 191

QY 165 EAEGEETELTTP 176
Db 192 LGGPGQLTYTTP 203
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RESULT 13
PGCA_BOVIN
ID PGCA_BOVIN STANDARD; PRT; 2364 AA.
AC P13608; P79117; Q28159;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
DE protein) (CSPCP).
GN AGC1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hering T.M., Kollar J., Huynh T.D.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 563-1056 FROM N.A.
RX MEDLINE=89380219; PubMed=2528543;
RA Antonsson P., Heinegaard D., Oldberg A.;
RT "The keratan sulfate-enriched region of bovine cartilage proteoglycan
RT consists of a consecutively repeated hexapeptide motif.";
RL J. Biol. Chem. 264:16170-16173(1989).
RN [3]
RP SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.
RX MEDLINE=87270630; PubMed=3111460;
RA Oldberg A., Antonsson P., Heinegaard D.;
RT "The partial amino acid sequence of bovine cartilage proteoglycan,
RT deduced from a cDNA clone, contains numerous Ser-Gly sequences
RT arranged in homologous repeats.";
RL Biochem. J. 243:255-259(1987).
RN [4]
RP SEQUENCE OF 2114-2150 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=93352525; PubMed=8349621;
RA Fuelleop C., Walcz E., Valyon M., Glant T.T.;
RT "Expression of alternatively spliced epidermal growth factor-like
RT domains in aggregans of different species. Evidence for a novel
RT module.";
RL J. Biol. Chem. 268:17377-17383(1993).
RN [5]
RP PARTIAL SEQUENCE.
RX MEDLINE=85027710; PubMed=6489519;
RA Perin J.-P., Bonnet F., Jolles J., Jolles P.;
RT "Sequence data concerning the protein core of the cartilage
RT proteoglycan monomers. Characterization of a sequence allowing the
RT synthesis of an oligonucleotide probe.";
RL FEBS Lett. 176:37-42(1984).
RN [6]
RP PARTIAL SEQUENCE.
RX MEDLINE=87005253; PubMed=3530809;
RA Perin J.P., Bonnet F., Jolles P.;
RT "Structural relationship between link proteins and proteoglycan
RT monomers.";
RL FEBS Lett. 206:73-77(1986).
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
CC matrix of cartilaginous tissues. A major function of this protein
CC is to resist compression in cartilage. It binds avidly to
CC hyaluronic acid via an amino-terminal globular region. May play a
CC regulatory role in the matrix assembly of the cartilage.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P13608-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P13608-2; Sequence=VSP_003072;
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino

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CC terminus of the proteoglycan, while another globular region, G3,
CC makes up the C-terminus. G1 contains link domains and thus
CC consists of three disulfide-bonded loop structures designated as
CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
CC and the chondroitin sulfate (CS) attachment domains lie between G2
CC and G3.
CC -!- PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-
CC LINKED (ABOUT 40) OLIGOSACCHARIDES.
CC -!- PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN
CC ADULT AND FETAL BOVINE PROTEOGLYCANS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
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CC -----
CC EMBL; U76615; AAB38524.1; -
CC EMBL; L07053; -; NOT_ANNOTATED_CDS.
CC PIR; A34234; A39808.
CC PIR; T42630; T42630.
CC HSSP; P08709; 1BF9.
CC InterPro; IPR002353; Antifreeze1.
CC InterPro; IPR00152; Asx_hydroxyl_S.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR01881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR01304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR003324; SGXSG.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 1.
CC Pfam; PF00047; ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF02339; SGXSG; 61.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 4.
CC PRINTS; PR00356; ANTIFREEZE1.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 4.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00445; LINK; 4.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS00026; EGF_3; 1.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; FALSE_NEG.
CC PROSITE; PS01241; LINK; 4.
CC Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
CC Calcium; Alternative splicing; Repeat; Immunoglobulin domain.
CC SIGNAL 1 16 POTENTIAL.
CC CHAIN 17 2364 AGGECAN CORE PROTEIN.
CC DOMAIN 25 147 IG-LIKE V-TYPE.
CC DOMAIN 170 247 LINK 1.
CC DOMAIN 268 349 LINK 2.
CC DOMAIN 504 581 LINK 3.
CC DOMAIN 602 683 LINK 4.
CC DOMAIN 774 907 23 X 6 AA APPROXIMATE TANDEM REPEATS OF

```


RL Immunity 10:691-700(1999).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/Sv; TISSUE=Endothelial cells, and Spleen;

RX MEDLINE=99359842; PubMed=10430665;

RA Norworthy P.J., Taylor P.R., Walport M.J., Botto M.;

RT "Cloning of the mouse homolog of the 126-kDa human C1q/MBL/SP-A receptor, C1qRp.";

RL Mamm. Genome 10:789-793(1999).

CC -!- FUNCTION: Receptor (or element of a larger receptor complex) for C1q, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in intercellular adhesion. Marker for early multipotent hematopoietic precursor cells. May play a role in cell-cell interactions during hematopoietic and vascular development.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed in lung, heart and bone marrow. Expressed at lower level in ovary, whole embryo and fetal liver. Not detected in brain, adult liver or thymus. Highly expressed in peritoneal cavity and bone marrow macrophages. Not detected in epithelial cells.

CC -!- DEVELOPMENTAL STAGE: First detectable in day 9 embryos, in the endocardium and vascular endothelium in the anterior part of the embryo. Expression in endothelial cells, initially restricted to aorta, omphalomesenteric and umbilical arteries, later extends to subcardinal veins, intersomitic arteries and perimeural vessels. On day 10, detectable in the entire embryo.

CC -!- PTM: N- and O-glycosylated (By similarity).

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

CC -!- SIMILARITY: Contains 5 EGF-like domains.

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CC -----

CC EMBL; AF074856; AAC63274.1; -.

CC EMBL; AF081789; AAC62649.1; -.

CC EMBL; AF099939; AAD47906.1; -.

CC EMBL; AF099938; AAD47906.1; JOINED.

CC HSSP; P35555; 1EMN.

CC MGD; MGI:106664; Clqrl.

CC GO; GO:0016023; C:cytoplasmic vesicle; IDA.

CC GO; GO:0016021; C:integral to membrane; ISS.

CC GO; GO:0005886; C:plasma membrane; IDA.

CC GO; GO:0004872; F:receptor activity; ISS.

CC GO; GO:0016337; P:cell-cell adhesion; ISS.

CC GO; GO:0042116; P:macrophage activation; ISS.

CC GO; GO:0006909; P:phagocytosis; ISS.

CC InterPro; IPR000152; Asx hydroxyl_S.

CC InterPro; IPR001881; EGF_Ca.

CC InterPro; IPR006209; EGF_like.

CC InterPro; IPR001304; Lectin_C.

CC Pfam; PF00008; EGF; 5.

CC Pfam; PF00059; lectin_c; 1.

CC SMART; SM00034; CLECT; 1.

CC SMART; SM00179; EGF_CA; 3.

CC PROSITE; PS00010; ASX_HYDROXYL; 3.

CC PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.

CC PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.

CC PROSITE; PS01186; EGF_2; 3.

CC PROSITE; PS50026; EGF_3; 4.

CC PROSITE; PS01187; EGF_CA; 3.

CC PROSITE; PS01187; EGF_CA; 3.

KW Cell adhesion; Receptor; Repeat; Signal; Transmembrane;

KW EGF-like domain; Lectin; Glycoprotein.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 644 COMPLEMENT COMPONENT C1Q RECEPTOR.

FT DOMAIN 23 572 EXTRACELLULAR (POTENTIAL).

FT

FT TRANSMEM 593 573 594 644 POTENTIAL.

FT DOMAIN 31 173 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 257 298 C-TYPE LECTIN.

FT DOMAIN 299 341 EGF-LIKE 1.

FT DOMAIN 342 381 EGF-LIKE 2.

FT DOMAIN 382 423 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 424 465 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

FT DISULFID 261 272 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

FT DISULFID 268 282 BY SIMILARITY.

FT DISULFID 284 297 BY SIMILARITY.

FT DISULFID 303 314 BY SIMILARITY.

FT DISULFID 308 325 BY SIMILARITY.

FT DISULFID 327 340 BY SIMILARITY.

FT DISULFID 346 355 BY SIMILARITY.

FT DISULFID 351 364 BY SIMILARITY.

FT DISULFID 366 380 BY SIMILARITY.

FT DISULFID 386 397 BY SIMILARITY.

FT DISULFID 393 406 BY SIMILARITY.

FT DISULFID 408 422 BY SIMILARITY.

FT DISULFID 428 440 BY SIMILARITY.

FT DISULFID 436 449 BY SIMILARITY.

FT DISULFID 451 464 BY SIMILARITY.

FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 322 322 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 644 AA; 69354 MW; EB4351648BF8635A CRC64;

Query Match 14.0%; Score 153.5; DB 1; Length 644;

Best Local Similarity 24.1%; Pred. No. 4.2e-06;

Matches 51; Conservative 32; Mismatches 70; Indels 59; Gaps 11;

QY 3 LSGQP-----VCRGGTQPCYKVIYFHDTSRLNFEFAKACRRDGGQLVSIES 51

Db 13 LLGQPWAGAAADSQAVVCEG---TACYTAHW-----GKLSAAEAQHRCNENGNLATVKS 64

QY 52 EDEQKLEKFIENLLPSD-----GDFWGLRRREKQSNSTACQDL-----YAWT-DGS 99

Db 65 EEEARHVQQAQLTQLKTKAPLEAKMGKFWIGLQR---EKGNCITYHDLPMRGFSWVGGE 120

QY 100 ISQFRNRY-VDEPSCGSEVCVMY-----HQPSAPAGIGGYPYFQWDDRC----- 144

Db 121 DTAYSNWYKASKSSCIFKRCVSLILDLSLTPHPSHLP-----KWHESPCGTPEAPG 171

QY 145 NMKNFICKYSDEKPAVPSREAEGETELTTP 176

Db 172 NSIEGFLCKFNFKGMCRLALGGPGRVYTTTP 203

RESULT 18

PGCA_RAT

ID PGCA_RAT STANDARD; PRT; 2124 AA.

AC P07897;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE AggreCAN core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).

GN AGC1 OR AGC.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=101116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88087070; PubMed=36933370;

RA Doege K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.;

RT "Complete primary structure of the rat cartilage proteoglycan core protein deduced from cDNA clones.";

RL J. Biol. Chem. 262:17757-17767(1987).

RN [2]

RP REVISION TO 698.

RA Doege K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.;

RL J. Biol. Chem. 263:10040-10040(1988).

RN [3] SEQUENCE OF 1856-2124 FROM N.A.
RP MEDLINE=86250698; PubMed=2424893;
RX Doerge K., Fernandez P., Hassell J.R., Sasaki M., Yamada Y.;
RA "Partial cDNA sequence encoding a globular domain at the C terminus
RT of the rat cartilage proteoglycan";
RL J. Biol. Chem. 261:8108-8111(1986).
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
CC matrix of cartilaginous tissues. A major function of this protein
CC is to resist compression in cartilage. It binds avidly to
CC hyaluronic acid via an amino-terminal globular region. May play a
CC regulatory role in the matrix assembly of the cartilage.
CC -!- SUBUNIT: Interacts with FBLN1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
CC terminus of the proteoglycan, while another globular region, G3,
CC makes up the COOH terminus. G1 contains link domains and thus
CC consists of three disulfide-bonded loop structures designated as
CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
CC and the chondroitin sulfate (CS) attachment domains lie between G2
CC and G3.
CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate
CC chains, N-linked and O-linked oligosaccharides.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M13518; AAA41836.1; .
CC EMBL; J03485; AAA21000.1; ALT_SEQ.
CC PIR; A92623; A28452.
CC HSSP; P98066; 1TSG.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR003324; SGXXSG.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00047; ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF02339; SGXXSG; 55.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 4.
CC PRINTS; PR00356; ANTIFREEZEII.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 4.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00406; IGV; 1.
CC SMART; SM00445; LINK; 4.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC PROSITE; PS01241; LINK; 4.
KW Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; Repeat;
KW Immunoglobulin domain.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 2124 AGGECAN CORE PROTEIN.
FT DOMAIN 34 147 IG-LIKE V-TYPE.
FT DOMAIN 170 247 LINK 1.

FT DOMAIN 268 349 LINK 2.
FT DOMAIN 504 581 LINK 3.
FT DOMAIN 602 683 LINK 4.
FT DOMAIN 1910 2036 C-TYPE LECTIN.
FT DOMAIN 2040 2098 SUSHI.
FT DOMAIN 48 140 G1-A.
FT DOMAIN 152 247 G1-B.
FT DOMAIN 253 349 G1-B'.
FT DOMAIN 486 580 G2-B.
FT DOMAIN 587 682 G2-B'.
FT DOMAIN 685 798 KS.
FT DOMAIN 801 1226 CS-1.
FT DOMAIN 1227 1909 CS-2.
FT DOMAIN 1910 2124 G3.
FT DISULFID 51 133 BY SIMILARITY.
FT DISULFID 175 246 BY SIMILARITY.
FT DISULFID 199 220 BY SIMILARITY.
FT DISULFID 273 348 BY SIMILARITY.
FT DISULFID 297 318 BY SIMILARITY.
FT DISULFID 509 580 BY SIMILARITY.
FT DISULFID 533 554 BY SIMILARITY.
FT DISULFID 607 682 BY SIMILARITY.
FT DISULFID 631 652 BY SIMILARITY.
FT DISULFID 1914 1925 BY SIMILARITY.
FT DISULFID 1942 2034 BY SIMILARITY.
FT DISULFID 2010 2026 BY SIMILARITY.
FT DISULFID 2041 2084 BY SIMILARITY.
FT DISULFID 2070 2097 BY SIMILARITY.
FT CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 667 667 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1842 1842 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 2124 AA; 221117 MW; E30BBE61593A34B1 CRC64;

Query Match 14.0%; Score 153.5; DB 1; Length 2124;
Best Local Similarity 26.3%; Pred. No. 1.8e-05;
Matches 47; Conservative 27; Mismatches 62; Indels 43; Gaps 9;

QY 6 QPVCRGG---TQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVLSIESDEQKLEKFI 62
Db 1911 QECCGEGWTKFQGHCYR--HFPD---RETWVDAERRCRCQQSHLSSIVTPEQEFVNKVA 1965

QY 63 ENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWYVDEP----SCGSEV 117
Db 1966 Q-----DYQWIGL-----NDRITGDFRWSGDGHSLOFEKWRPNQPDNFFATGEDC 2010

QY 118 CVVMYHQPSAPAGIGGYPYFQWNDRCNMKNFICKYS----DEKPAVPSRAEGEETE 172
Db 2011 VVMWHERG-----EWNDVPCNYQLPFTCKKGTGTVACGEPPAVEHARTLGQKGD 2058

RESULT 19
PGCB BOVIN
ID PGCB_BOVIN STANDARD; PRT; 912 AA.
AC Q28062;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Brevican core protein precursor.
GN BCAN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94193597; PubMed=8144512;
RA Yamada H., Watanabe K., Shimonaka M., Yamaguchi Y.;


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EMBL; X75887; CAA53481.1; -.
PIR; A54423; A54423.
HSSP; P20693; 1HLJ.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR000742; EGF_2.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IBGF.
InterPro; IPR007110; IG-like.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_v.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 1.
Pfam; PF00047; ig; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
PRINTS; PR00356; ANTIFREEZEII.
PRINTS; PR01265; LINKMODULE.
ProDom; PD000918; Link; 2.
SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
SMART; SM00406; IGv; 1.
SMART; SM00445; LINK; 2.
PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Hyaluronic acid; Proteoglycan; Lectin; Signal; Sushi;
EGF-like domain; Repeat; Immunoglobulin domain.
SIGNAL 1 22 POTENTIAL.
CHAIN 23 912 BREVICAN CORE PROTEIN.
DOMAIN 36 155 IG-LIKE V-TYPE.
DOMAIN 174 251 LINK 1.
DOMAIN 272 353 LINK 2.
DOMAIN 647 683 EGF-LIKE.
DOMAIN 683 811 C-TYPE LECTIN.
DOMAIN 812 876 SUSHI.
DOMAIN 57 137 BY SIMILARITY.
DISULFID 179 250 BY SIMILARITY.
DISULFID 203 224 BY SIMILARITY.

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RESULT 20
CD93 HUMAN
ID CD93 HUMAN STANDARD; PRT; 652 AA.
AC Q9NPY3; O0274;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Complement component C1q receptor precursor (Complement component 1, q
DE subcomponent, receptor 1) (ClqRp) (ClqR(p)) (Clq/MBL/SPA receptor)
DE (CD93 antigen) (CDw93).
GN CLQR1 OR CD93.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97199258; PubMed=9047234;
RA Nepomuceno R.R., Henschen-Edman A.H., Burgess W.H., Tenner A.J.;
RT "CDNA cloning and primary structure analysis of ClqR(P), the human
RT Clq/MBL/SPA receptor that mediates enhanced phagocytosis in vitro.";
RL Immunity 6:119-129(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT ALA-318.
RX MEDLINE=21640567; PubMed=11781389;
RA Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N.,
RA Prager E., Staefler G., Madic O., Stockinger H., Knapp W.;
RT "Identification of human CD93 as the phagocytic C1q receptor (ClqRp)
RT by expression cloning.";
RL J. Leukoc. Biol. 71:133-140(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levaeslao M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeb H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=21990337; PubMed=11994479;
RA McGreal E.P., Ikewaki N., Akatsu H., Morgan B.P., Gasque P.,
RT "Human Clqrp is identical with CD93 and the mni-11 antigen but does
RT not bind Clq.";
RL J. Immunol. 168:5222-5232(2002).
RN [6]
RP O-GLYCOSYLATION.
RX MEDLINE=99192777; PubMed=10092817;
RA Nepomuceno R.R., Ruiz S., Park M., Tenner A.J.,
RT "Clqrp is a heavily O-glycosylated cell surface protein involved in
RT the regulation of phagocytic activity.";
RL J. Immunol. 162:3583-3589(1999).
CC -!- FUNCTION: Receptor (or element of a larger receptor complex) for
CC Clq, mannose-binding lectin (MBL2) and pulmonary surfactant
CC protein A (SPA). May mediate the enhancement of phagocytosis in
CC monocytes and macrophages upon interaction with soluble defense
CC collagens. May play a role in intercellular adhesion.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in endothelial cells,
CC platelets, cells of myeloid origin, such as monocytes and
CC neutrophils. Not expressed in cells of lymphoid origin.
CC -!- PTM: N- and O-glycosylated.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 5 EGF-like domains.
CC -!- CAUTION: Has been sometimes referred to as a collectin receptor.
CC -!- CAUTION: According to Ref.5, Clq is not a ligand for ClqR1.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 3:1-6(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/46724656_g.htm".

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U94333; AAB53110.1; -;
CC EMBL; AL118508; CAC00597.1; -;
CC EMBL; BC028075; AAH28075.1; -;
CC HSSP; P35555; 1EMN.
CC Genew; HGNC:15855; ClQR1.
CC MIM; 120577; -;
CC GO; GO:0016021; C:integral to membrane; IC.
CC GO; GO:004872; F:receptor activity; NAS.
CC GO; GO:0016337; P:cell-cell adhesion; IDA.
CC GO; GO:0042116; P:macrophage activation; NAS.
CC GO; GO:0006909; P:phagocytosis; NAS.
CC InterPro; IPR001152; Asx_hydroxyl_S.
CC InterPro; IPR011881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR01304; Lectin_C.
CC Pfam; PF00008; EGF; 5.
CC Pfam; PF00059; lectin_c; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 3.
CC PROSITE; PS0010; ASX_HYDROXYL; 3.
CC PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
CC PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS0026; EGF_3; 3.
CC PROSITE; PS01187; EGF_CA; 3.
KW Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
KW EGF-like domain; Lectin; Glycoprotein; Polymorphism.
FT SIGNAL 1 21 COMPLEMENT COMPONENT ClQ RECEPTOR.
FT CHAIN 22 652 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 24 580 POTENTIAL.
FT TRANSMEM 581 601 POTENTIAL.
FT DOMAIN 602 652 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 174 C-TYPE LECTIN.
FT DOMAIN 260 301 EGF-LIKE 1.
FT DOMAIN 302 344 EGF-LIKE 2.
FT DOMAIN 345 384 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 385 426 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 427 468 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 594 601 POLY-LEU.
FT DISULFID 264 275 BY SIMILARITY.
FT DISULFID 271 285 BY SIMILARITY.
FT DISULFID 287 300 BY SIMILARITY.
FT DISULFID 306 317 BY SIMILARITY.
FT DISULFID 311 328 BY SIMILARITY.
FT DISULFID 330 343 BY SIMILARITY.
FT DISULFID 349 358 BY SIMILARITY.
FT DISULFID 354 367 BY SIMILARITY.
FT DISULFID 369 383 BY SIMILARITY.
FT DISULFID 389 400 BY SIMILARITY.
FT DISULFID 396 409 BY SIMILARITY.
FT DISULFID 411 425 BY SIMILARITY.
FT DISULFID 431 443 BY SIMILARITY.
FT DISULFID 439 452 BY SIMILARITY.
FT DISULFID 454 467 BY SIMILARITY.
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 318 318 V -> A.
FT CONFLICT 22 22 /FTID=VAR_013573.
FT CONFLICT 36 36 T -> V (IN REF. 1; AA SEQUENCE).
FT CONFLICT 38 39 C -> T (IN REF. 1; AA SEQUENCE).
FT CONFLICT 155 155 TA -> RI (IN REF. 1; AA SEQUENCE).
FT CONFLICT 186 186 S -> N (IN REF. 1).
FT CONFLICT 186 186 G -> A (IN REF. 1; AA SEQUENCE).
FT CONFLICT 492 492 S -> A (IN REF. 1; AA SEQUENCE).
FT CONFLICT 496 496 R -> Q (IN REF. 1; AA SEQUENCE).
FT CONFLICT 504 504 R -> G (IN REF. 1; AA SEQUENCE).
FT CONFLICT 504 504

```
FT CONFLICT 541 541 P -> S (IN REF. 1).
SQ SEQUENCE 652 AA; 68560 MW; EECA0FEAC55FCAC2 CRC64;

Query Match 13.8%; Score 151.5; DB 1; Length 652;
Best Local Similarity 24.4%; Pred. No. 6.4e-06;
Matches 50; Conservative 38; Mismatches 74; Indels 43; Gaps 9;

QY 2 LLSGP-----VCRGGTQPCYKVIYFHDTSRRLNFEFAKEACRRDGGQLVSI 50
Db 13 LLTQPGAGTGADTEAVCVG---TACYTA-----HSGKLSAAEAQNHCNQGNTATVK 64

QY 51 SEDEQKLEKFIENLLPSD-----GDFWIGLRRREKQSNSTACQDLYAWT-DGSISQ 102
Db 65 SKEEAQHVRVLAQLLRREAAALTARMSKFWIGLQREKGCCLDPSLPLKGFVWGGEDTP 124

QY 103 FRNWWVD-EPSCGSEVCVVM---YHQPSAPAGIGGPPYMFQWDDRCNMKN---FI 151
Db 125 YSNWHKELRNSCISKRCVSLLLDLSQPLPSRLP-----KWSEGPCGSPGSPGSGNIEGFV 179

QY 152 KYSDEKPAVPSREAEGETELTTP 176
Db 180 CKFSFKGCMRPLALCGPGQVTTYTP 204
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RESULT 21
CLE1_HUMAN
ID -CLE1_HUMAN STANDARD; PRT; 197 AA.
AC O75596;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-type lectin superfamily member 1 precursor (Cartilage-derived C-type lectin).
GN CLECSF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=99453719; PubMed=10524194;
RA Neame P.J., Tapp H., Grimm D.R.;
RT "The cartilage-derived, C-type lectin (CLECSF1): structure of the gene and chromosomal location."
RL Biochim. Biophys. Acta 1446:193-202(1999).
CC -!- TISSUE SPECIFICITY: Restricted to cartilage.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
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CC -----
DR EMBL; AF077345; AAD12542.1; -.
DR EMBL; AF077344; AAD12542.1; JOINED.
DR HSSP; P05452; IHTN.
DR Genew; HGNC:2052; CLECSF1.
DR GO; GO:0005530; F:lectin; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR001304; lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 197 C-TYPE LECTIN SUPERFAMILY MEMBER 1.
FT DOMAIN 74 192 C-TYPE LECTIN.
FT DISULFID 68 78 BY SIMILARITY.
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FT DISULFID 95 191 BY SIMILARITY.
FT DISULFID 167 183 BY SIMILARITY.
SQ SEQUENCE 197 AA; 22232 MW; BB924DBDB7729A4 CRC64;

Query Match 13.7%; Score 151; DB 1; Length 197;
Best Local Similarity 25.0%; Pred. No. 1.6e-06;
Matches 38; Conservative 26; Mismatches 64; Indels 24; Gaps 4;

QY 6 QPVCRGGTQ--RPGYKVIYFHDTSRRLNFEFAKEACRRDGGQLVSISEDEQKLEKFI 63
Db 65 QTVCLRGTKVHKCYLA-----SEGLKHFHEANEDCISKGGILVPRNSDEINALQDYGK 119

QY 64 NLLPSDGDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCVVMYH 123
Db 120 RSLPGVNDFWLGI-----NDMVTEGKFPVDVNGIAISFLNWDRAQPNGGKRENCVLFS 171

QY 124 QPSAPAGIGGPPYMFQWDDRCNMKNFICKYS 155
Db 172 QSA-----QGWKSDACRSKRYICEFT 194
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RESULT 22
FCE2_HUMAN
ID -FCE2_HUMAN STANDARD; PRT; 321 AA.
AC P06734;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Low affinity immunoglobulin epsilon FC receptor (Lymphocyte Ige receptor) (FC-epsilon-RII) (CD23) (BLAST-2) (Immunoglobulin E-binding factor).
GN FCE2 OR IGEBF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87118255; PubMed=2949326;
RA Ikuta K., Takami M., Kim C.W., Honjo T., Miyoshi T., Tagaya Y., Kawabe T., Yodoi J.;
RT "Human lymphocyte Fc receptor for Ige: sequence homology of its cloned cDNA with animal lectins."
RL Proc. Natl. Acad. Sci. U.S.A. 84:819-823(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87051737; PubMed=28777743;
RA Kikutani H., Inui S., Sato R., Barsumian E.L., Owaki H., Yamasaki K., Kaisho T., Uchibayashi N., Hardy R.R., Hirano T., Tsunasawa S., Sakiyama F., Suemura M., Kishimoto T.;
RT "Molecular structure of human lymphocyte receptor for immunoglobulin E."
RL Cell 47:657-665(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218454; PubMed=3034567;
RA Luedin C., Hofstetter H., Sarfati M., Levy C.A., Suter U., Alaimo D., Kilcherr E., Frost H., Delespesse G.;
RT "Cloning and expression of the cDNA coding for a human lymphocyte Ige receptor."
RL EMBO J. 6:109-114(1987).
RN [4]
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=93038513; PubMed=1417742;
RA Rose K., Turcatti G., Graber P., Pochon S., Regamey P.-O., Jansen K.U., Magnenat E., Aubonne N., Bonnefoy J.-Y.;
RT "Partial characterization of natural and recombinant human soluble CD23."
RL Biochem. J. 286:819-824(1992).
RN [5]
RP ALTERNATIVE SPLICING.
RX MEDLINE=89028672; PubMed=2972386;
RA Yokota A., Kikutani H., Tanaka T., Sato R., Barsumian E.L.,
```

RA Suemura M., Kishimoto T.;
RT "Two species of human Fc epsilon receptor II (Fc epsilon RII/CD23):
RT tissue-specific and IL-4-specific regulation of gene expression.";
RL Cell 55:611-618(1988).
RN [6]
RP 3D-STRUCTURE MODELING OF LECTIN DOMAIN.
RX MEDLINE=94191542; PubMed=8142907;
RA Padlan E.A., Helm B.A.;
RT "Modeling of the lectin-homology domains of the human and murine low-
RT affinity Fc epsilon receptor (Fc epsilon RII/CD23).";
RL Receptor 3:325-341(1993).
RN [7]
RP 3D-STRUCTURE MODELING OF 173-285.
RX MEDLINE=96276216; PubMed=8745401;
RA Bajorath J., Aruffo A.;
RT "Structure-based modeling of the ligand binding domain of the human
RT cell surface receptor CD23 and comparison of two independently
RT derived molecular models.";
RL Protein Sci. 5:240-247(1996).
CC -!- FUNCTION: This receptor has essential roles in the regulation of
CC IgE production and in the differentiation of B-cells (it is a B-
CC cell-specific antigen).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS A
CC SOLUBLE EXCRETED FORM.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P06734-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P06734-2; Sequence=VSP_003057;
CC -!- PTM: N- and O-glycosylated.
CC -!- MISCELLANEOUS: There are two kinds of Fc receptors for IgE, which
CC differ in both structure and function: high affinity receptors on
CC basophils and mast cells and low affinity receptors on lymphocytes
CC and monocytes.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD23 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd23.htm".
CC -----
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CC -----
CC EMBL; M15059; AAA52434.1; -
CC EMBL; M14766; AAA52435.1; -
CC EMBL; X04772; CAA28465.1; -
CC EMBL; M23562; AAA52433.1; -
CC PIR; A26067; LNHUER.
CC PDB; 1HLI; 31-JAN-94.
CC PDB; 1KJE; 03-APR-96.
CC Genew; HGNC:3612; FCER2.
CC MIM; 151445; -
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005178; F:integrin binding; TAS.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR001304; Lectin_C.
CC Pfam; PF00059; lectin c; 1.
CC PRINTS; PR00356; ANTIFREEZEII.
CC SMART; SM00034; CLECT; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
CC Receptor; Antigen; IgE-binding protein; Repeat; Signal-anchor;
KW Transmembrane; Lectin; Glycoprotein; Alternative splicing;
KW 3D-structure.
KW CHAIN 1 321 MEMBRANE BOUND FORM.
FT CHAIN 150 321 SOLUBLE FORM.
FT CHAIN 1 21 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT TRANSMEM 22 47 (POTENTIAL).

FT DOMAIN 48 321 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 162 284 C-TYPE LECTIN (LONG FORM).
FT SITE 149 CLEAVAGE.
FT REPEAT 69 89
FT REPEAT 90 110
FT REPEAT 111 131
FT DISULFID 160 288
FT DISULFID 163 174
FT DISULFID 191 282
FT DISULFID 259 273
FT CARBOHYD 63 7
FT VARSPLIC 1 7
FT
FT CONFLICT 269
FT STRAND 174 193
FT HELIX 184 195
FT TURN 194 198
FT STRAND 197 216
FT HELIX 204 215
FT TURN 215 228
FT STRAND 219 230
FT TURN 229 234
FT STRAND 231 236
FT TURN 235 239
FT STRAND 239 245
FT STRAND 245 248
FT TURN 247 255
FT TURN 254 262
FT STRAND 259 265
FT TURN 264 271
FT STRAND 268 274
FT TURN 273 284
FT STRAND 281 284
SQ SEQUENCE 321 AA; 36468 MW; F86708C0E6515B87 CRC64;

Query Match 13.5%; Score 149; DB 1; Length 321;
Best Local Similarity 30.2%; Pred. No. 4.5e-06;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

QY 14 QRPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIIEDEQKLEKFIENLLPSDGFV 73
Db 171 QRKCY---YFGKGTKQ--WHARYACDDMEGQLVSIHSPEEQDFTLTKH-----ASHTGSW 220
QY 74 IGLRRREEKQSNSTACQDLYAWTDGSIISQFRNWWYVDPSGCS--EVCVVMYHQPSAPAGI 131
Db 221 IGLRLDLKGE-----FIWVDGSHVDYSNWPAGPEPTSRSGQEDCVMM-----RGS 265
QY 132 GGPYMFQWDDRCNMK--NNFICKYSDKPAV---PSRAEAGE-----ETELTPV 177
Db 266 G-----RWNDAFCDRLKLGAWVC-----DRLATCTPPASEGSAESMGPSRDPDGRLPPTS 316
QY 178 LP 179
Db 317 AP 318

RESULT 23
PGCA_MOUSE
ID PGCA_MOUSE STANDARD; PRT; 2132 AA.
AC Q61282; Q64021;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE AggreCan core protein precursor (Cartilage-specific proteoglycan core
DE protein) (CSPCP).
GN AGC1 OR AGC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Cartilage;

RX MEDLINE=95104847; PubMed=7806222;
RA Walcz E., Deak F., Erhardt P., Coulter S.N., Fueleop C., Horvath P.,
RA Doege K.J., Glant T.T.;
RT "Complete coding sequence, deduced primary structure, chromosomal
RT localization, and structural analysis of murine aggrecan.";
RL Genomics 22:364-371(1994).
RN [2]
RP SEQUENCE OF 211-326 FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=95004579; PubMed=7920633;
RA Watanabe H., Kimata K., Line S., Strong D., Gao L.-Y., Kozak C.A.,
RA Yamada Y.;
RT "Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in
RT the aggrecan gene.";
RL Nat. Genet. 7:154-157(1994).
RN [3]
RP INTERACTION WITH FBLN1.
RX MEDLINE=99329059; PubMed=10400671;
RA Asberg A., Adam S., Kostka G., Timpl R., Heinegaard D.;
RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
RT versican.";
RL J. Biol. Chem. 274:20444-20449(1999).
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
CC matrix of cartilaginous tissues. A major function of this protein
CC is to resist compression in cartilage. It binds avidly to
CC hyaluronic acid via an amino-terminal globular region. May play a
CC regulatory role in the matrix assembly of the cartilage.
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
CC terminus of the proteoglycan, while another globular region, G3,
CC makes up the COOH terminus. G1 contains link domains and thus
CC consists of three disulfide-bonded loop structures designated as
CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
CC and the chondroitin sulfate (CS) attachment domains lie between G2
CC and G3.
CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate
CC chains, N-linked and O-linked oligosaccharides.
CC -!- DISEASE: Defects in AGC1 are the cause of cartilage matrix
CC deficiency (CMD). CMD is an autosomal recessive syndrome
CC characterized by cleft palate, short limbs, tail and snout.
CC Mutation in strain CMD causes absence of aggrecan by truncation of
CC the protein (mutation in the G1 domain).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
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CC -----
CC EMBL; L07049; AAC37670.1; --
CC EMBL; S73722; AAB32160.1; --
CC EMBL; S73721; AAB32160.1; JOINED.
CC PIR; A55182; A55182.
CC HSSP; P98066; 1TSG.
CC MGD; MGI:99602; Agcl.
CC InterPro; IPR002353; Antifreeze2.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_v.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR003324; SGXSG.
CC InterPro; IPR00436; Sushi_SCR_CCP.

DR Pfam; PF00047; ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF02339; SGXSG; 60.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; Xlink; 4.
DR PRINTS; PRO0356; ANTIFREEZE2.
DR PRINTS; PRO1265; LINKMODULE.
DR ProDom; PD000918; Link; 4.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00445; LINK; 4.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS01241; LINK; 4.
KW Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; Repeat;
KW immunoglobulin domain.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 2132 AGGREGAN CORE PROTEIN.
FT DOMAIN 34 147 IG-LIKE V-TYPE.
FT DOMAIN 170 247 LINK 1.
FT DOMAIN 268 349 LINK 2.
FT DOMAIN 504 581 LINK 3.
FT DOMAIN 602 683 LINK 4.
FT DOMAIN 1918 2044 C-TYPE LECTIN.
FT DOMAIN 2048 2106 SUSHI.
FT DOMAIN 48 140 G1-A.
FT DOMAIN 152 247 G1-B.
FT DOMAIN 253 349 G1-B'.
FT DOMAIN 486 580 G2-B.
FT DOMAIN 587 682 G2-B'.
FT DOMAIN 685 803 KS.
FT DOMAIN 805 1231 CS-1.
FT DOMAIN 1232 1917 CS-2.
FT DOMAIN 1917 2132 G3.
FT DISULFID 51 133 BY SIMILARITY.
FT DISULFID 175 246 BY SIMILARITY.
FT DISULFID 199 220 BY SIMILARITY.
FT DISULFID 273 348 BY SIMILARITY.
FT DISULFID 297 318 BY SIMILARITY.
FT DISULFID 509 580 BY SIMILARITY.
FT DISULFID 533 554 BY SIMILARITY.
FT DISULFID 607 682 BY SIMILARITY.
FT DISULFID 631 652 BY SIMILARITY.
FT DISULFID 1922 1933 BY SIMILARITY.
FT DISULFID 1950 2042 BY SIMILARITY.
FT DISULFID 2018 2034 BY SIMILARITY.
FT DISULFID 2049 2092 BY SIMILARITY.
FT DISULFID 2078 2105 BY SIMILARITY.
FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 667 667 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1675 1675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 1171 1173 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 2132 AA; 222008 MW; 0B2BCDFC6CBDA163 CRC64;

Query Match 13.4%; Score 147.5; DB 1; Length 2132;
Best Local Similarity 24.7%; Pred. No. 6.3e-05;
Matches 45; Conservative 30; Mismatches 64; Indels 43; Gaps 9;

QY 3 LSGQPVCRGG---TQPCYKVYFHDTSRLNFEEAKEACRRDGGQLVSEDEBQKLE 59
Db 1916 VADQEQQEEGWTQFQHCYR--HFPD---RETWVDAERCRREQQSHLSSIVTPEQEFTN 1970
QY 60 KFIENLLPSDGDFF-WIGLRREEKQSNSTACQDLYAWTDGSIQFRNWTYVDEP----SCG 114
Db 1971 KNAQ-----DYQWIGL-----NDRITGDFRWSGDGHSLSQFEKWRPNQDNFFATG 2015

QY 115 SEVCVVMYHQPSAPAGIGPYMFQWDDRCNMKNFNICKYS-----DEKPAVPSREAEGEE 170
Db 2016 EDCVVMWHERG-----EWNDVPCNYQLPFTCKKGTACGDPVVEHARTLGQK 2064
QY 171 TE 172
Db 2065 KD 2066

RESULT 24
PGCB_MOUSE STANDARD; PRT; 883 AA.
ID PGCB_MOUSE
AC Q61361;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Brevican core protein precursor.
GN BCAN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=97432816; PubMed=9286696;
RA Rauch U., Meyer H., Brakebusch C., Seidenbecher C., Gundelfinger E.D.,
RA Beier D.R., Fassler R.;
RT "Sequence and chromosomal localization of the mouse brevican gene.";
RL Genomics 44:15-21(1997).
CC -!- FUNCTION: May play a role in the terminally differentiating and
CC the adult nervous system during postnatal development. Could
CC stabilize interactions between HA and brain proteoglycans.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Brain (By similarity).
CC -!- PTM: Contains mostly chondroitin sulfate (By similarity).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
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CC -----
DR EMBL; X87096; CAA60575.1; -.
DR PIR; S57653; S57653.
DR HSSP; P20693; 1HLJ.
DR MGD; MGI:1096385; Bcan.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; xlink; 2.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR01265; LINKMODULE.

DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS01241; LINK; 2.
KW Glycoprotein; Hyaluronic acid; Proteoglycan; Lectin; Signal; Sushi;
KW EGF-like domain; Repeat; Immunoglobulin domain.
FT SIGNAL 1 22
FT CHAIN 23 883
FT DOMAIN 35 154
FT DOMAIN 173 250
FT DOMAIN 271 352
FT DOMAIN 622 658
FT DOMAIN 658 786
FT DOMAIN 787 851
FT DISULFID 56 136
FT DISULFID 178 249
FT DISULFID 202 223
FT DISULFID 276 351
FT DISULFID 300 321
FT DISULFID 626 637
FT DISULFID 631 646
FT DISULFID 648 657
FT DISULFID 664 675
FT DISULFID 692 784
FT DISULFID 760 776
FT DISULFID 791 834
FT DISULFID 820 847
FT CARBOHYD 129 129
FT CARBOHYD 336 336
SQ SEQUENCE 883 AA; 96013 MW; CC2C33C97B453E45 CRC64;
Query Match 13.4%; Score 147; DB 1; Length 883;
Best Local Similarity 29.7%; Pred. No. 2.4e-05;
Matches 43; Conservative 21; Mismatches 45; Indels 36; Gaps 8;
QY 14 QRPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSEDEBQKLI-EKFIENLLPSDGF 72
Db 672 QGACYK---HFSTR-SWEAEQCRALGAHLTSICTPEEQDFVNDRYEQ----- 719
QY 73 WIGLRRREKQSNSTACQDLVATDGSISQFRNWWYVDEPS---CGSEVCVVM-YHQPSAP 128
Db 720 WIGL-----NDRTIEGDFLWSDGAPLLYENWNPQPDSPYLSGNCVVMVWHDQG-- 769
QY 129 AGIGGYPYMFQWDDRCNMKNFNICK 153
Db 770 -----QWSDVPCNYHLSYTC 785

RESULT 25
PGCA_CHICK
ID PGCA_CHICK STANDARD; PRT; 2109 AA.
AC P07898; Q90810; Q90820; Q90991; Q91047;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
DE protein) (CSPCP).
GN AGCI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Embryo;
RX MEDLINE=94043149; PubMed=8226878;
RA Li H., Schwartz N.B., Vertel B.M.;
RT "cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core
RT protein and identification of a stop codon in the aggrecan gene
RT associated with the chondrodystrophy, nanomelia.";
RL J. Biol. Chem. 268:23504-23511(1993).
RN [2]
RP SEQUENCE OF 1042-1559 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=90307744; PubMed=1694853;
RA Krueger R.C. Jr., Fields T.A., Mensch J.R. Jr., Schwartz N.B.;
RT "Chick cartilage chondroitin sulfate proteoglycan core protein. II.
RT Nucleotide sequence of cDNA clone and localization of the S103L
RT epitope.";
RL J. Biol. Chem. 265:12088-12097(1990).
RN [3]
RP SEQUENCE OF 1-1855 AND 1893-2109 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=93111968; PubMed=1339285;
RA Chandrasekaran L., Tanzer M.L.;
RT "Molecular cloning of chicken aggrecan. Structural analyses.";
RL Biochem. J. 288:903-910(1992).
RN [4]
RP ERRATUM.
RX MEDLINE=94107258; PubMed=8280087;
RA Chandrasekaran L., Tanzer M.L.;
RL Biochem. J. 296:885-887(1993).
RN [5]
RP SEQUENCE OF 1492-1610 FROM N.A.
RC STRAIN=White leghorn; TISSUE=Chondrocytes;
RX MEDLINE=95128519; PubMed=7827752;
RA Primorac D., Stover M.L., Clark S.H., Rowe D.W.;
RT "Molecular basis of nanomelia, a heritable chondrodystrophy of
RT chicken.";
RL Matrix Biol. 14:297-305(1994).
RN [6]
RP SEQUENCE OF 1894-2109 FROM N.A.
RX MEDLINE=89008500; PubMed=3170613;
RA Tanaka T., Har-El R., Tanzer M.L.;
RT "Partial structure of the gene for chicken cartilage proteoglycan
RT core protein.";
RL J. Biol. Chem. 263:15831-15835(1988).
RN [7]
RP SEQUENCE OF 1693-1855 AND 1893-2109 FROM N.A.
RX MEDLINE=86259736; PubMed=3460082;
RA Sai S., Tanaka T., Koshier R.A., Tanzer M.L.;
RT "Cloning and sequence analysis of a partial cDNA for chicken
RT cartilage proteoglycan core protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5081-5085(1986).
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
CC matrix of cartilaginous tissues. A major function of this protein
CC is to resist compression in cartilage. It binds avidly to
CC hyaluronic acid via an amino-terminal globular region. May play a
CC regulatory role in the matrix assembly of the cartilage.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P07898-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P07898-2; Sequence=VSP_003073;
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
CC terminus of the proteoglycan, while another globular region, G3,
CC makes up the COOH terminus. G1 contains link domains and thus
CC consists of three disulfide-bonded loop structures designated as
CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
CC and the chondroitin sulfate (CS) attachment domains lie between G2
CC and G3.
CC -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate

CC chains, N-linked and O-linked oligosaccharides.
CC -!- DISEASE: DEFECTS IN AGC1 ARE THE CAUSE OF NANOMELIA, A LETHAL
CC CONNECTIVE TISSUE DISORDER AFFECTING CARTILAGE DEVELOPMENT
CC (CHONDRODYSTROPHY) CHARACTERIZED BY SHORTENED AND MALFORMED LIMBS.
CC AGGREGAN IS TRUNCATED AT ITS C-TERMINAL IN THE CS-2 BINDING DOMAIN
CC AND IS NOT ANYMORE SECRETED FROM THE CHONDROCYTES.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L21913; AAB19128.1; -.
CC EMBL; M38187; AAA48731.1; -.
CC EMBL; M88101; -; NOT ANNOTATED_CDS.
CC EMBL; S74657; AAC60751.1; -.
CC EMBL; S74656; AAC60751.1; JOINED.
CC EMBL; J04028; AAA48719.1; -.
CC EMBL; M13993; AAA48720.1; -.
CC PIR; I50421; I50421.
CC HSSP; P08709; 1BF9.
CC InterPro; IPR002353; AntifreezeII.
CC InterPro; IPR000152; Asx hydroxyl_s.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link.
CC InterPro; IPR003324; SGXSG.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 1.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF02339; SGXSG; 56.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 4.
CC PRINTS; PR00356; ANTIFREEZEII.
CC PRINTS; PR01265; LINKMODULE.
CC PRODOM; PD000918; Link; 4.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00445; LINK; 4.
CC PROSITE; PS00010; ASX HYDROXYL; 1.
CC PROSITE; PS00615; C_TYPE LECTIN_1; 1.
CC PROSITE; PS50041; C_TYPE LECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS50026; EGF_3; 1.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC PROSITE; PS01241; LINK; 4.
CC Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
KW Alternative splicing; Repeat; Immunoglobulin domain.
KW SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 2109 AGGREGAN CORE PROTEIN.
FT DOMAIN 34 143 IG-LIKE V-TYPE.
FT DOMAIN 166 243 LINK 1.
FT DOMAIN 264 346 LINK 2.
FT DOMAIN 537 614 LINK 3.
FT DOMAIN 635 716 LINK 4.
FT DOMAIN 1363 1742 19 X 20 AA TANDEM-REPEAT.

FT	DOMAIN	1855	1892	EGF-LIKE.
FT	DOMAIN	1901	2019	C-TYPE LECTIN.
FT	DOMAIN	2023	2081	SUSHI.
FT	DOMAIN	48	137	G1-A.
FT	DOMAIN	148	243	G1-B.
FT	DOMAIN	249	346	G1-B'.
FT	DOMAIN	519	613	G2-B.
FT	DOMAIN	620	715	G2-B'.
FT	DOMAIN	718	803	KS.
FT	DOMAIN	805	1264	CS-1.
FT	DOMAIN	1265	1742	CS-2.
FT	DOMAIN	1893	2109	G3.
FT	DISULFID	51	129	BY SIMILARITY.
FT	DISULFID	171	242	BY SIMILARITY.
FT	DISULFID	195	216	BY SIMILARITY.
FT	DISULFID	269	345	BY SIMILARITY.
FT	DISULFID	293	314	BY SIMILARITY.
FT	DISULFID	542	613	BY SIMILARITY.
FT	DISULFID	566	587	BY SIMILARITY.
FT	DISULFID	640	715	BY SIMILARITY.
FT	DISULFID	664	685	BY SIMILARITY.
FT	DISULFID	1859	1870	BY SIMILARITY.
FT	DISULFID	1864	1879	BY SIMILARITY.
FT	DISULFID	1881	1890	BY SIMILARITY.
FT	DISULFID	1897	1908	BY SIMILARITY.
FT	DISULFID	1925	2017	BY SIMILARITY.
FT	DISULFID	1993	2009	BY SIMILARITY.
FT	DISULFID	2024	2067	BY SIMILARITY.
FT	DISULFID	2053	2080	BY SIMILARITY.
FT	CARBOHYD	76	76	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	122	122	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	330	330	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	388	388	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	439	439	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	644	644	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	700	700	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	765	765	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	801	801	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	1856	1892	Missing (in isoform 2).
FT				/FTid=VSP_003073.
FT	CONFLICT	362	362	E -> D (IN REF. 3).
Query Match 13.3%; Score 146; DB 1; Length 2109;				
Best Local Similarity 25.0%; Pred. No. 8.5e-05;				
Matches 42; Conservative 28; Mismatches 58; Indels 40; Gaps 8;				
Qy	14	QRPCKVIYFHDTSRLNPFEEAKEACRRDGGQLVLSIESEDEQKLIKFIENLLPSDGDGDF-	72	
Db	1905	QCHCYR--HFEE---RETWMDAESRCREHQAHLSIIITPEEQEFVNSHAQ-----DYQ	1952	
Qy	73	WIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWNVYDEPS-----CGSEVCVVMYHQPSAP	128	
Db	1953	WIGLSDR-----AVENDFRWSDGHSLSQFENWRPNQPDNFFAFAGEDCVVMIWHEQG--	2002	
Qy	129	AGIGGPYMFQWNDRCNMKNNFICKYS-----DEKPAVPSREAEGETE	172	
Db	2003	-----EWNDVPCNYHLPFTCKKGTGTVACGDPVPVENARTFGRKKD	2041	
Search completed: September 9, 2004, 22:54:13				
Job time : 16.9631 secs				

Blank Sheet

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:48:35 ; Search time 24.9386 Seconds
(without alignments)
782.999 Million cell updates/sec

Title: US-09-887-855-2_COPY_25_227
Perfect score: 1100
Sequence: 1 RLLSGQPVCRGGTQRPCYKV.....EEDAKKTFKESREAAINLAY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl1:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	182	16.5	1456	1 A36563	mannose receptor p
2	178.5	16.2	1455	1 A48925	mannose receptor p
3	177	16.1	1268	2 S52781	neurocan - mouse
4	174.5	15.9	1643	2 T14274	versican precursor
5	174.5	15.9	3381	2 T42389	versican precursor
6	174	15.8	1257	2 S28764	neurocan precursor
7	174	15.8	2397	1 A55535	versican precursor
8	174	15.8	2409	1 A60979	versican precursor
9	171	15.5	3562	2 A47171	chondroitin sulfat
10	170.5	15.5	1479	2 T42710	mannose receptor,
11	158.5	14.4	1340	2 A39808	proteoglycan core
12	158.5	14.4	2327	2 T42630	aggrecan - bovine
13	158.5	14.4	2415	1 A39086	aggrecan precursor
14	154.5	14.0	612	2 B42755	E-selectin precurs
15	153.5	14.0	2124	2 A28452	proteoglycan core
16	152	13.8	912	2 A54423	brevican precursor
17	149.5	13.6	459	2 T24425	hypothetical prote
18	149	13.5	321	1 LNHUER	IGF Fc receptor II
19	148.5	13.5	330	2 T46256	brevican - human (
20	148	13.5	253	2 E89130	protein F52E1.2 [i
21	147.5	13.4	2132	1 A55182	aggrecan precursor
22	147	13.4	883	2 S57653	brevican precursor
23	146.5	13.3	162	1 LNRCL	lectin BRA3-1 prec
24	146	13.3	2109	1 I50421	aggrecan precursor
25	145.5	13.2	742	2 JC7595	scavenger receptor
26	145	13.2	883	2 S49126	brevican precursor
27	144.5	13.1	173	2 S10548	lectin - barnacle
28	144.5	13.1	372	2 S23936	L-selectin precurs
29	144.5	13.1	404	2 A46274	HIV gp120-binding

30	143.5	13.0	129	2 JC4329	coagulation factor
31	143.5	13.0	372	1 A32375	L-selectin precurs
32	143.5	13.0	463	2 T26655	hypothetical prote
33	142.5	13.0	131	2 JC5058	bitiscetin alpha c
34	142	12.9	1487	2 S48719	phospholipase-A(2)
35	141.5	12.9	331	1 LNMSE	IGF Fc receptor, 1
36	140.5	12.8	162	1 LNRCL	lectin BRA3-2 prec
37	140	12.7	370	2 S22124	L-selectin precurs
38	139	12.6	248	1 LNHUPS	pulmonary surfacta
39	139	12.6	248	1 LNHUP6	pulmonary surfacta
40	139	12.6	248	1 LNHUP1	pulmonary surfacta
41	139	12.6	283	1 LNFHLS	lectin precursor -
42	138.5	12.6	152	2 JC4690	coagulation factor
43	138.5	12.6	202	2 JC4031	tetranectin precur
44	138	12.5	280	2 T29200	hypothetical prote
45	137.5	12.5	309	1 S34198	IGF Fc receptor II

ALIGNMENTS

RESULT 1

A36563
mannose receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A36563; A60926; A44255; B44255; C44255; D44255; F44255; G44255; H44
R:Taylor, M.E.; Conary, J.T.; Lennartz, M.R.; Stahl, P.D.; Drickamer, K.
J. Biol. Chem. 265, 12156-12162, 1990
A:Title: Primary structure of the mannose receptor contains multiple motifs resembling c
A:Reference number: A36563; MUID:90324192; PMID:2373685
A:Accession: A36563
A:Molecule type: mRNA
A:Residues: 1-1456 <TAY>
A:Cross-references: GB:J05550; NID:g188675; PIDN:AAA59868.1; PID:g188676
A:Note: parts of this sequence, including the amino end of the mature protein, were conf
R:Ezekowitz, R.A.B.; Sastry, K.; Bailly, P.; Warner, A.
J. Exp. Med. 172, 1785-1794, 1990
A:Title: Molecular characterization of the human macrophage mannose receptor: demonstrat
A:Reference number: A60926; MUID:91079783; PMID:2258707
A:Accession: A60926
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1333,'T',1335-1456 <EZE>
A:Cross-references: GB:X55635
A:Note: translation of the nucleotide sequence is incomplete
A:Note: in the authors' translation additional residues Pro-Glu-Ile are shown after 497-
R:Kim, S.J.; Ruiz, N.; Bezouska, K.; Drickamer, K.
Genomics 14, 721-727, 1992
A:Title: Organization of the gene encoding the human macrophage mannose receptor (MRC1).
A:Reference number: A44255; MUID:93052405; PMID:1294118
A:Accession: A44255
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 155-233,'KSAL',238-283;346-428;492-569;631-714,716-719;783-820,'N',822-865;'
A:Note: sequence extracted from NCBI backbone (NCBIP:118415, NCBIP:118421, NCBIP:118428,
C:Genetics:
A:Gene: GDB:MRC1
A:Cross-references: GDB:133759; OMIM:153618
A:Map position: 10p13-10p13
C:Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C:Keywords: duplication; lectin; tandem repeat; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;168-209/Domain: fibronectin type II repeat homology <2F1>
F;223-340/Domain: C-type lectin homology <LCH1>
F;362-486/Domain: C-type lectin homology <LCH2>
F;945-1079/Domain: C-type lectin homology <LCH3>

Query Match 16.5%; Score 182; DB 1; Length 1456;
Best Local Similarity 25.5%; Pred. No. 8.3e-08;
Matches 52; Conservative 37; Mismatches 61; Indels 54; Gaps 8;

QY ·18 YKVIYFHDTSRRLNFEAKEACRRDGGQLVSISEDEQKLIKFIENLLPSDGFWIGLR 77

Db 807 YKDYQYFSEKETMDNARAFCKRNFGLVSIQSESEKKFLWKYV-NRNDASAYFIGLL 865

QY 78 RREEKQSNSTACQDLYAWTDGSGISQFRNMYVDEPSCGS--EVCVMYHQPSAPAGIGPY 135

Db 866 ISLDKK-----FAWMDGSKVDYVSWATGEPNFANEDENCVTMY-----SNSGF----- 908

QY 136 MFQWNDRCNMKNFICKYSDEK----PAVPSREAEGEETELTPVLPEETQE----- 184

Db 909 ---WINDINGYPNAPICQRHNSINATVMP-----TWPSVPSGCKEGWNFYSN 954

QY 185 -----EDAKKTFKESREAAAL 199

Db 955 KCFKIFGFMEERKNWQEARACI 978

RESULT 2

A48925

mannose receptor precursor, macrophage - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A48925; S21320; PC2245

R;Harris, N.; Super, M.; Rits, M.; Chang, G.; Ezekowitz, R.A.

Blood 80, 2363-2373, 1992

A;Title: Characterization of the murine macrophage mannose receptor: demonstration that

A;Reference number: A48925; MUID:93043353; PMID:1421407

A;Accession: A48925

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-1455 <HAR>

A;Experimental source: peritoneal macrophage

A;Note: sequence extracted from NCBI backbone (NCBIP:118733)

R;Harris, N.; Super, M.; Rits, M.; Chang, G.; Ezekowitz, R.B.

submitted to the EMBL Data Library, April 1992

A;Description: Characterization of the murine macrophage mannose receptor: Demonstration

on.

A;Reference number: S21320

A;Accession: S21320

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-302,'W',303-1117,'E',1119-1455 <HA2>

A;Cross-references: EMBL:Z11974; NID:G52997; PIDN:CAA78028.1; PID:G52998

R;Harris, N.; Peters, L.L.; Eicher, E.M.; Rits, M.; Raspberry, D.; Eichbaum, Q.G.; Super

Biochem. Biophys. Res. Commun. 198, 682-692, 1994

A;Title: The exon-intron structure and chromosomal localization of the mouse macrophage

A;Reference number: PC2245; MUID:94128116; PMID:8297379

A;Accession: PC2245

A;Molecule type: mRNA

A;Residues: 35-105 <HA3>

C;Genetics:

A;Gene: Mrc1

A;Map position: 2

C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re

C;Keywords: membrane protein; receptor

F;168-209/Domain: fibronectin type II repeat homology <2F9>

F;361-485/Domain: C-type lectin homology <LCH1>

F;943-1077/Domain: C-type lectin homology <LCH2>

Query Match 16.2%; Score 178.5; DB 1; Length 1455;

Best Local Similarity 25.9%; Pred. No. 1.7e-07;

Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;

QY 18 YKVIYFHDTSRRLNFEAEACRRDGGQLVSIIESEDEQKLEKFIENLLPSDGFWIGLR 77

Db 806 YKDYQYFSEKETMDNARAFCKRNFGLVSIQSESEKKFLWKYI-NKNGGQSPYFIGML 864

QY 78 RREEKQSNSTACQDLYAWTDGSGISQFRNMYVDEPSCGS--EVCVMYHQPSAPAGIGPY 135

Db 865 ISMDKK-----FIWMDGSKVDYVSWATGEPNFANDDENCVTMY-----TNSGF----- 907

QY 136 MFQWNDRCNMKNFICK---YSDEKPAVPSREAEGEETELTPVLPEETQE----- 184

Db 908 ---WINDINGYPNAPICQRHNSINATAMP-----TPTTFFGCKEGWHLKYNK 953

QY 185 -----EDAKKTFKESREAAALNL 201

Db 954 CFKIFGFANEKKSWQDARQACKGL 978

RESULT 3

S52781

neurocan - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000

C;Accession: S52781

R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.

submitted to the EMBL Data Library, February 1995

A;Description: Amino acid sequence of mouse neurocan and brevican and their different ex

A;Reference number: S52781

A;Accession: S52781

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1268 <RAU>

A;Cross-references: EMBL:X84727; NID:G758629; PIDN:CAA59216.1; PID:G758630

C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF

F;176-253/Domain: link protein repeat homology <LNK1>

F;274-355/Domain: link protein repeat homology <LNK2>

F;964-995/Domain: EGF homology <EGF>

F;1040-1160/Domain: C-type lectin homology <LCH>

F;1167-1223/Domain: complement factor H repeat homology <PHD>

Query Match 16.1%; Score 177; DB 2; Length 1268;

Best Local Similarity 31.5%; Pred. No. 2e-07;

Matches 45; Conservative 17; Mismatches 49; Indels 32; Gaps 6;

QY 14 QRPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSIIESEDEQKLEKFIENLLPSDGFDFW 73

Db 1048 QGHCYR--YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW 1096

QY 74 IGLRRREKQSNSTACQDLYAWTDGSGISQFRNMYVDEPS---CGSEVCVMYHQPSAPAG 130

Db 1097 IGLNDRITVERD-----FQWTDNTGLQYENWREKQPDNFFAGGDCVVMVAHESG--- 1145

QY 131 IGGPYMFQWNDRCNMKNFICK 153

Db 1146 -----RWNDVPCNPNLPYVCK 1161

RESULT 4

T14274

versican precursor, splice form V2 - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000

C;Accession: T14274

R;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.

J. Biol. Chem. 273, 15758-15764, 1998

A;Title: Versican V2 is a major extracellular matrix component of the mature bovine brain

A;Reference number: Z17954; MUID:98288320; PMID:9624174

A;Accession: T14274

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1643 <SCH>

A;Cross-references: EMBL:AF060458; NID:G3253303; PID:G3253304; PIDN:AAC24360.1

A;Experimental source: brain

C;Keywords: glycoprotein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-1643/Product: versican, splice form V2 #status predicted <MAT>

F;57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 15.9%; Score 174.5; DB 2; Length 1643;

Best Local Similarity 25.5%; Pred. No. 4.4e-07;

Matches 59; Conservative 26; Mismatches 71; Indels 75; Gaps 11;

QY 14 QRPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSIIESEDEQKLEKFIENLLPSDGFDF- 72

Db 1424 QGQCYK--YF---AHRRTWDAARECECLQGAHLTSILSHEEQMFVNRV-----GHDIQ 1471

QY 73 WIGLRRREEKQNSTACQDLYAWTDGSIQFRNWWYDEP-----SCGSEVCVVMYHQPSAP 128
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 1472 WIGL-----NDKMFEDHFRWTDGSTLQYENWRPNQDPSFFSTGDCVVIWHENG-- 1521
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
QY 129 AGIGGPFMFQWDDRCNMKNFICKYS----DEKPAVPSREAEGE----- 169
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 1522 -----QWNDVPCNYHLTYTCKGTVACGQPPVVENAKTFGKMKPRYEINSLIRYHC 1572
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
QY 170 -----ETELTT-----PVL-----PEETQEEEDAKKTFKESREAAALN 200
:
Db 1573 KDGFIQRLHPTIRCLNGRWAMPKITCLNPSAYQRTYSKKYFKNSSSAKDN 1623
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

RESULT 5
T42389
versican precursor, splice form V0 - bovine
N/Alternate names: chondroitin sulfate proteoglycan
C/Species: Bos primigenius taurus (cattle)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000
C/Accession: T42389
R/Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 15758-15764, 1998
A/Title: Versican V2 is a major extracellular matrix component of the mature bovine brain
A/Reference number: Z17954; MUID:98288320; PMID:9624174
A/Accession: T42389
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-3381 <SCH>
A/Cross-references: EMBL:AF060456; NID:g3253299; PID:g3253300; PIDN:AAC24358.1
C/Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin
C/Keywords: chondroitin sulfate proteoglycan; extracellular matrix; glycoprotein
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-3381/Product: versican, splice form V0 #status predicted <MAT>
F/57,331,352,817,965,1017,1333,1393,1437,1463,1653,1974,2045,2074,2103,2263,2290,2356,26

Query Match 15.9%; Score 174.5; DB 2; Length 3381;
Best Local Similarity 25.5%; Pred. No. 1e-06;
Matches 59; Conservative 26; Mismatches 71; Indels 75; Gaps 11;

QY 14 QRPCYKVIYFHDTSRLNFEERAKEACRRDGGQLVSIIESEDEQKLIKFIENLLPSDGDGF- 72
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 3162 QGQCYK--YF---AHRRTWDAARECRLOGAHLTSILSHEEQMFVNRV-----GHDYQ 3209
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

QY 73 WIGLRRREEKQNSTACQDLYAWTDGSIQFRNWWYDEP-----SCGSEVCVVMYHQPSAP 128
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 3210 WIGL-----NDKMFEDHFRWTDGSTLQYENWRPNQDPSFFSTGDCVVIWHENG-- 3259
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

QY 129 AGIGGPFMFQWDDRCNMKNFICKYS----DEKPAVPSREAEGE----- 169
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 3260 -----QWNDVPCNYHLTYTCKGTVACGQPPVVENAKTFGKMKPRYEINSLIRYHC 3310
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

QY 170 -----ETELTT-----PVL-----PEETQEEEDAKKTFKESREAAALN 200
:
Db 3311 KDGFIQRLHPTIRCLNGRWAMPKITCLNPSAYQRTYSKKYFKNSSSAKDN 3361
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

RESULT 6
S28764
neurocan precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C/Accession: S28764
R/Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K.
J. Biol. Chem. 267, 19536-19547, 1992
A/Title: Cloning and primary structure of neurocan, a developmentally regulated, aggrega
A/Reference number: S28764; MUID:92406907; PMID:1326557
A/Accession: S28764
A/Molecule type: mRNA
A/Residues: 1-1257 <RAU>
A/Cross-references: EMBL:M97161; NID:g205649; PIDN:AAC37679.1; PID:g205650
C/Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C/Keywords: chondroitin sulfate proteoglycan; glycoprotein

F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-1257/Product: neurocan #status predicted <MAT>
F/176-253/Domain: link protein repeat homology <LNK1>
F/274-355/Domain: link protein repeat homology <LNK2>
F/364-366/Region: cell attachment (R-G-D) motif
F/953-984/Domain: EGF homology <EGF>
F/1029-1149/Domain: C-type lectin homology <LCH>
F/1156-1212/Domain: complement factor H repeat homology <FHD>
F/121,339,737,967,1164/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F/944/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental

Query Match 15.8%; Score 174; DB 2; Length 1257;
Best Local Similarity 30.8%; Pred. No. 3.6e-07;
Matches 44; Conservative 18; Mismatches 49; Indels 32; Gaps 6;

QY 14 QRPCYKVIYFHDTSRLNFEERAKEACRRDGGQLVSIIESEDEQKLIKFIENLLPSDGDGF 73
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 1037 QGHCYR--YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW 1085
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

QY 74 IGLRRREEKQNSTACQDLYAWTDGSIQFRNWWYDEPS---CGSEVCVVMYHQPSAPAG 130
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 1086 IGLNDRTVRD-----FQWTDNTGLQYENWRKQPDNFFAGGEDCVVMVAHENG--- 1134
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

QY 131 IGGPFMFQWDDRCNMKNFICK 153
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 1135 -----RWNDVPCNYNLPYCK 1150
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

RESULT 7
A55535
versican precursor - mouse
N/Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
versican
N/Contains: glial hyaluronate-binding protein
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: A55535
R/Rito, K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K.
J. Biol. Chem. 270, 958-965, 1995
A/Title: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generate
A/Reference number: A55535; MUID:95122551; PMID:7822336
A/Accession: A55535
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-2397 <RES>
A/Cross-references: GB:D16263; NID:g862460; PIDN:BAA03796.1; PID:g862461
C/Superfamily: versican; C-type lectin homology; complement factor H repeat homology; EG
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-1654/Domain: versican #status predicted <MAT>
F/167-244/Domain: link protein repeat homology <LNK1>
F/265-346/Domain: link protein repeat homology <LNK2>
F/2095-2126/Domain: EGF homology <EG1>
F/2133-2164/Domain: EGF homology <EG2>
F/2171-2291/Domain: C-type lectin homology <LCH>
F/2298-2354/Domain: complement factor H repeat homology <FHD>

Query Match 15.8%; Score 174; DB 1; Length 2397;
Best Local Similarity 28.5%; Pred. No. 7.6e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;

QY 14 QRPCYKVIYFHDTSRLNFEERAKEACRRDGGQLVSIIESEDEQKLIKFIENLLPSDGDGF- 72
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 2179 QGQCYK--YF---AHRRTWDAARECRLOGAHLTSILSHEEQMFVNRV-----GHDYQ 2226
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

QY 73 WIGLRRREEKQNSTACQDLYAWTDGSIQFRNWWYDEP---SCGSEVCVVMYHQPSAP 128
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 2227 WIGL-----NDKMFEDHFRWTDGSLQYENWRPNQDPSFFSAGEDCVVIWHENG-- 2276
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

QY 129 AGIGGPFMFQWDDRCNMKNFICKYS---DEKPAVPSREAEGE 169
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |
Db 2277 -----QWNDVPCNYHLTYTCKGTVACGQPPVVENAKTFGK 2312
| | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : |

RESULT 8
A60979
versican precursor - human
N;Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
N;Contains: glial hyaluronate-binding protein
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 19-Jan-2001
C;Accession: S06014; S43921; A60979; A30358; A29348; A45131; I54179
R;Zimmermann, D.R.; Ruoslahti, E.
EMBO J. 8, 2975-2981, 1989
A;Title: Multiple domains of the large fibroblast proteoglycan, versican.
A;Reference number: S06014; MUID:90059882; PMID:2583089
A;Accession: S06014
A;Molecule type: mRNA
A;Residues: 1-2409 <ZIM>
A;Cross-references: GB:X15998; NID:G37662; PIDN:CAA34128.1; PID:G37663
R;Yao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
A;Title: Identification of the proteoglycan versican in aorta and smooth muscle cells by
A;Reference number: S43921; MUID:95005762; PMID:7921538
A;Accession: S43921
A;Molecule type: mRNA
A;Residues: 208-440;1094-1385;1910-2246 <YAO>
R;Bignami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
Brain Res. Bull. 22, 67-70, 1989
A;Title: Structural similarity of hyaluronate binding proteins in brain and cartilage.
A;Reference number: A60979; MUID:89229983; PMID:2469524
A;Accession: A60979
A;Molecule type: protein
A;Residues: 171-210;289-303 <BIG>
R;Perides, G.; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
J. Biol. Chem. 264, 5981-5987, 1989
A;Title: Isolation and partial characterization of a glial hyaluronate-binding protein.
A;Reference number: A30358; MUID:89174663; PMID:2466833
A;Accession: A30358
A;Molecule type: protein
A;Residues: 24-50;80-87,'D',89-119;128-155;167-218;229-259,'IR',261-268;277-283,'G',285-
R;Krusius, T.; Gehlsen, K.R.; Ruoslahti, E.
J. Biol. Chem. 262, 13120-13125, 1987
A;Title: A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like
A;Reference number: A29348; MUID:88007514; PMID:2820964
A;Accession: A29348
A;Molecule type: mRNA
A;Residues: 1725,'V',1727-2409 <KRU>
A;Cross-references: GB:J02814
R;Perides, G.; Rahemtulla, F.; Lane, W.S.; Asher, R.A.; Bignami, A.
J. Biol. Chem. 267, 23883-23887, 1992
A;Title: Isolation of a large aggregating proteoglycan from human brain.
A;Reference number: A45131; MUID:93054750; PMID:1429726
A;Contents: brain
A;Accession: A45131
A;Molecule type: protein
A;Residues: 21-22,'X',24-37 <PE2>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118884)
R;Iozzo, R.V.; Naso, M.F.; Cannizzaro, L.A.; Wasmuth, J.J.; McPherson, J.D.
Genomics 14, 845-851, 1992
A;Title: Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chro
A;Reference number: I54179; MUID:93122792; PMID:1478664
A;Accession: I54179
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 251-347 <RES>
A;Cross-references: GB:S52488; NID:G263313; PIDN:AAB24878.1; PID:G263314
C;Genetics:
A;Gene: GDB:CSPG2
A;Cross-references: GDB:127873; OMIM:118661
A;Map position: 5q12-5q14
C;Superfamily: versican; C-type lectin homology; complement factor H repeat homology; EG
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-2409/Product: proteoglycan 24K core protein #status predicted <MAT>
F;167-244/Domain: link protein repeat homology <LNK1>

F;265-346/Domain: link protein repeat homology <LNK2>
F;559-1654/Domain: chondroitin sulfate attachment #status predicted <GAG>
F;2106-2137/Domain: EGF homology <EG1>
F;2144-2175/Domain: EGF homology <EG2>
F;2182-2302/Domain: C-type lectin homology <LCH>
F;2309-2365/Domain: complement factor H repeat homology <FHD>
Query Match 15.8%; Score 174; DB 1; Length 2409;
Best Local Similarity 28.5%; Pred. No. 7.6e-07;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
QY 14 QRPCYKVIYFHDTSRRRLNFEEAKEACRRDGGQLVSIIESEDEQKLEKFIENLLPSDGF- 72
Db 2190 QGQCYK--YF---AHRRTWDAARECRLOGAHLTSILSHEEQVFNRV-----GHDYQ 2237
QY 73 WIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEP-----SCGSEVCVVMYHQPSP 128
Db 2238 WIGL-----NDKMFHDFRWTGDTLQYENWRPNQPDSPFSAGDCVVIWHENG-- 2287
QY 129 AGIGGPFYMFQWDDRCNMKNFICKYS---DEKPAVPSREAE 169
Db 2288 -----QWNDVPCNYHLTYTCKKGTACGQPPVVENAKTFGK 2323
RESULT 9
A47171
chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text change 21-Jul-2000
C;Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during
A;Reference number: A47171; MUID:93300846; PMID:8314802
A;Accession: A47171
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-3562 <SHI>
A;Cross-references: NID:G391643; PIDN:BAA02742.1; PID:G391644
A;Experimental source: stage 22-23 developing limb buds
A;Note: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457)
C;Superfamily: chicken chondroitin sulfate proteoglycan <LNK1>
F;166-243/Domain: link protein repeat homology <LNK1>
F;264-345/Domain: link protein repeat homology <LNK2>
F;3258-3289/Domain: EGF homology <EGF1>
F;3296-3327/Domain: EGF homology <EGF>
F;3334-3454/Domain: C-type lectin homology <LCH>
F;3461-3517/Domain: complement factor H repeat homology <FHD>
Query Match 15.5%; Score 171; DB 2; Length 3562;
Best Local Similarity 28.5%; Pred. No. 2.2e-06;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;
QY 14 QRPCYKVIYFHDTSRRRLNFEEAKEACRRDGGQLVSIIESEDEQKLEKFIENLLPSDGF- 72
Db 3342 QGQCYK--YF---AHRRTWDTAARECRLOGAHLTSILSHEEQVFNRI-----GHDYQ 3389
QY 73 WIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEP-----SCGSEVCVVMYHQPSP 128
Db 3390 WIGL-----NDKMFERDFRWTGSPLOQYENWRPNQPDSPFSAGDCVVIWHENG-- 3439
QY 129 AGIGGPFYMFQWDDRCNMKNFICKYS---DEKPAVPSREAE 169
Db 3440 -----QWNDVPCNYHLTYTCKKGTACGQPPVVENAKTFGK 3475
RESULT 10
T42710
mannose receptor, macrophage - mouse
N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 09-Jun-2000

C;Accession: T42710
R;Wu, K.; Yuan, J.; Lasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996
A;Title: Characterization of a novel member of the macrophage mannose receptor type C le
A;Reference number: Z22235; MUID:96355501; PMID:8702911
A;Accession: T42710
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1479 <WUK>
A;Cross-references: EMBL:US6734; NID:g1336073; PID:g1336074; PIDN:AAC52729.1
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C;Keywords: membrane protein; receptor
F;186-227/Domain: fibronectin type II repeat homology <2FR>

Query Match 15.5%; Score 170.5; DB 2; Length 1479;
Best Local Similarity 31.4%; Pred. No. 8.8e-07;
Matches 48; Conservative 22; Mismatches 48; Indels 35; Gaps 7;

QY 4 SGQPVCRGGTQRPCYKVIYFHDTSRRLLNFEEAKEACRRDGGQLVSISEDEQKLIKFI 63
Db 384 SWQPF-----QGHCYRL-----QAERKSWQESKRACLRGGGDLLSIHMAELEFITKQIK 433

QY 64 NLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS---CGSEVCVV 120
Db 434 QEVE---ELWIGL-----NDLKLQMNFEWSDGSLVSFTTHWHPFPNFRDLSLEDCVT 482

QY 121 MYHQPSAPAGIGGPFYMFQWNDRCNMKNFICK 153
Db 483 IW-----GPEG-----RWNDSPCNQSLPSICK 504

RESULT 11
A39808
proteoglycan core protein, cartilage - bovine (fragments)
N;Alternate names: aggrecan; aggregating cartilage proteoglycan
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Mar-1992 #sequence revision 23-Mar-1995 #text change 13-Aug-1999
C;Accession: A34234; A27752; A39808; A27751; E29164; B27751; D27751; E27751; F27
R;Antonsen, P.; Heinegard, D.; Oldberg, A.
J. Biol. Chem. 264, 16170-16173, 1989
A;Title: The keratan sulfate-enriched region of bovine cartilage proteoglycan consists o
A;Reference number: A34234; MUID:89380219; PMID:2528543
A;Accession: A34234
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 128-621 <ANT>
A;Cross-references: GB:J05028
R;Oldberg, A.; Antonsen, P.; Heinegard, D.
Biochem. J. 243, 255-259, 1987
A;Title: The partial amino acid sequence of bovine cartilage proteoglycan,deduced from a
A;Reference number: A27752; MUID:87270630; PMID:3111460
A;Accession: A27752
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 622-1340 <OLD>
R;Sandy, J.D.; Boynton, R.E.; Flannery, C.R.
J. Biol. Chem. 266, 8198-8205, 1991
A;Title: Analysis of the catabolism of aggrecan in cartilage explants by quantitation of
A;Reference number: A39808; MUID:91217051; PMID:2022637
A;Accession: A39808
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28;59-82;131-137,'QSET',142-149;196-207;226-249;1137-1143;1252-1267;1274-1
R;Perin, J.P.; Bonnet, F.; Jolles, P.
FEBS Lett. 206, 73-77, 1986
A;Title: Structural relationship between link proteins and proteoglycan monomers.
A;Reference number: A27751; MUID:87005253; PMID:3530809
A;Accession: A27751
A;Molecule type: protein
A;Residues: 29-58;74-130;174-175,'A',177-204;208-225 <PER>
R;Perin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.
FEBS Lett. 176, 37-42, 1984
A;Title: Sequence data concerning the protein core of the cartilage proteoglycan monomer

A;Reference number: A91327; MUID:85027710; PMID:6489519
A;Accession: E29164
A;Molecule type: protein
A;Residues: 1230-1249 <PE2>
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: glycoprotein
F;8-28/Domain: link protein repeat homology (fragment) <LNK1>
F;29-58/Domain: link protein repeat homology (fragment) <LNK2>
F;80-146/Domain: link protein repeat homology (fragments) <LNK3>
F;167-248/Domain: link protein repeat homology <LNK4>
F;1130-1250/Domain: C-type lectin homology <LCH>
F;1257-1313/Domain: complement factor H repeat homology <FHD>

Query Match 14.4%; Score 158.5; DB 2; Length 1340;
Best Local Similarity 26.8%; Pred. No. 9.1e-06;
Matches 48; Conservative 29; Mismatches 59; Indels 43; Gaps 10;

QY 6 QPVCRRGG---TORPCYKVIYFHDTSRRLLNFEEAKEACRRDGGQLVSISEDEQKLIKFI 62
Db 1127 QKLCEEGWTKFQGHCYR--HFPD---RATWVDAESQCRKQQSHLSIVTPEQ----EFV 1177

QY 63 ENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP----SCGSEV 117
Db 1178 NN---NAQDYQWIGL-----NDKTIEGDFRWSGDGHSLSQFENWRPNQDNFFATGEDC 1226

QY 118 CVMVYHQPSAPAGIGGPFYMFQWNDRCNMKNFICKYS---DEKPAVPSRAEAGEETE 172
Db 1227 VVMWHEKG-----EWNDVPCNYQLPFTCKKGTACGEPVVEHARIFGQKKD 1274

RESULT 12
T42630
aggrecan - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C;Accession: T42630
R;Hering, T.M.; Kollar, J.; Huynh, T.D.
submitted to the EMBL Data Library, September 1996
A;Description: Complete coding sequence of bovine aggrecan: comparative structural analy
A;Reference number: Z22182
A;Accession: T42630
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2327 <HER>
A;Cross-references: EMBL:U76615; NID:g1730259; PID:g1730260; PIDN:AAB38524.1
A;Experimental source: articular chondrocytes
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycoprot

Query Match 14.4%; Score 158.5; DB 2; Length 2327;
Best Local Similarity 26.8%; Pred. No. 1.7e-05;
Matches 48; Conservative 29; Mismatches 59; Indels 43; Gaps 10;

QY 6 QPVCRRGG---TORPCYKVIYFHDTSRRLLNFEEAKEACRRDGGQLVSISEDEQKLIKFI 62
Db 2114 QKLCEEGWTKFQGHCYR--HFPD---RATWVDAESQCRKQQSHLSIVTPEQ----EFV 2164

QY 63 ENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP----SCGSEV 117
Db 2165 NN---NAQDYQWIGL-----NDKTIEGDFRWSGDGHSLSQFENWRPNQDNFFATGEDC 2213

QY 118 CVMVYHQPSAPAGIGGPFYMFQWNDRCNMKNFICKYS---DEKPAVPSRAEAGEETE 172
Db 2214 VVMWHEKG-----EWNDVPCNYQLPFTCKKGTACGEPVVEHARIFGQKKD 2261

RESULT 13
A39086
aggrecan precursor, cartilage long splice form [validated] - human
N;Alternate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan; p
N;Contains: aggrecan cartilage short splice form
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000

C;Accession: A39086; S50206; A43919; S46659; S66389; S68646; S62786; A34226; B43919; C43
R;Doegi, K.J.; Sasaki, M.; Kimura, T.; Yamada, Y.
J. Biol. Chem. 266, 894-902, 1991
A;Title: Complete coding sequence and deduced primary structure of the human cartilage I
A;Reference number: A39086; MUID:91093289; PMID:1985970
A;Accession: A39086
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2162,2201-2329,'A',2392-2415 <DOE>
A;Cross-references: GB:M55172; NID:g178258; PIDN:AAA62824.1; PID:g178259
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Accession: S50206
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 350-497 <GLU>
A;Cross-references: EMBL:X80278; NID:g516295
A;Note: this translation is not annotated in GenBank entry HSAGGREG, release 113.0
R;Sandy, J.D.; Flannery, C.R.; Neame, P.J.; Lohmander, L.S.
J. Clin. Invest. 89, 1512-1516, 1992
A;Title: The structure of aggrecan fragments in human synovial fluid. Evidence for the i
domain.
A;Reference number: A43919; MUID:92235266; PMID:1569188
A;Accession: A43919
A;Molecule type: protein
A;Residues: 361-370,'X',372-373;393-399,'X',401-407,'X',409 <SAN>
A;Cross-references: PIDN:AAB22079.1; PID:g248844; PIDN:AAB22077.1; PID:g248842; PIDN:AAH
A;Experimental source: synovial fluid
A;Note: sequences modified after extraction from NCBI backbone
R;Barry, F.P.; Neame, P.J.; Sasse, J.; Pearson, D.
Matrix Biol. 14, 323-328, 1994
A;Title: Length variation in the keratan sulfate domain of mammalian aggrecan.
A;Reference number: I46998; MUID:95128522; PMID:7827755
A;Accession: S46659
A;Molecule type: DNA
A;Residues: 764-765,'A',767-846,'V',848-862,'X',864 <BAR>
A;Cross-references: EMBL:S74659; NID:g807127; PIDN:AAC60643.1; PID:g807128
A;Note: the authors translated the codon GAA for residue 803 as Ala and Cyt for residue
R;Illic, M.Z.; Mok, M.T.; Williamson, O.D.; Campbell, M.A.; Hughes, C.E.; Handley, C.J.
Arch. Biochem. Biophys. 322, 22-30, 1995
A;Title: Catabolism of aggrecan by explant cultures of human articular cartilage in the
A;Reference number: S66389; MUID:96004775; PMID:7574678
A;Accession: S66389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 17-23;24,'X',26-27;393-401;402-403 <ILI>
R;Posang, A.J.; Last, K.; Knaeuper, V.; Murphy, G.; Neame, P.J.
FEBS Lett. 380, 17-20, 1996
A;Title: Degradation of cartilage aggrecan by collagenase-3 (MMP-13).
A;Reference number: S68646; MUID:96181659; PMID:8603731
A;Accession: S68646
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'V',404-405,'XX' <POS>
R;Dudhia, J.; Davidson, C.M.; Wells, T.M.; Vynios, D.H.; Hardingham, T.E.; Bayliss, M.T.
Biochem. J. 313, 933-940, 1996
A;Title: Age-related changes in the content of the C-terminal region of aggrecan in huma
A;Reference number: S62786; MUID:96190740; PMID:8611178
A;Accession: S62786
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1778-1927,'A',1929-1963,'V',1965-2162,2201-2415 <DUD>
A;Cross-references: EMBL:X17406; NID:g30248; PIDN:CAA35463.1; PID:g30249
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1990
R;Baldwin, C.T.; Reginato, A.M.; Prockop, D.J.
J. Biol. Chem. 264, 15747-15750, 1989
A;Title: A new epidermal growth factor-like domain in the human core protein for the lar
A;Reference number: A34226; MUID:89380154; PMID:2789216
A;Accession: A34226
A;Molecule type: mRNA
A;Residues: 1936-1963,'V',1965-2069,'A',2071-2415 <BAL>

A;Cross-references: GB:J05062; NID:g181167; PIDN:AAA35726.1; PID:g181168
C;Genetics:
A;Gene: GDB:AGC1; CSPG1; CSPGCP; MSK16
A;Cross-references: GDB:127479; OMIM:155760
A;Map position: 15q26-15q26
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF
C;Keywords: alternative splicing; cartilage; chondroitin sulfate proteoglycan; extracell
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-2415/Product: aggrecan cartilage long splice form #status predicted <MATL>
F;20-2162,2201-2415/Product: aggrecan cartilage short splice form #status predicted <MATN
F;20-2162,2201-2329,'A',2392-2415/Product: aggrecan short splice form #status predicted
F;44-135/Domain: immunoglobulin homology <IMM>
F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;495-572/Domain: link protein repeat homology <LNK3>
F;593-673/Domain: link protein repeat homology <LNK4>
F;677-861/Domain: keratan sulfate attachment #status predicted <KSA>
F;864-1510/Domain: chondroitin sulfate attachment #status predicted <CS1>
F;1511-2162/Domain: chondroitin sulfate attachment #status predicted <CS2>
F;2168-2198/Domain: EGF homology <EGF>
F;2205-2325/Domain: C-type lectin homology <LCH>
F;2332-2388/Domain: complement factor H repeat homology <FHD>
F;126,239,333,387,434,602,657,737,1898/Binding site: carbohydrate (Asn) (covalent) #statu
F;371,376/Binding site: keratan sulfate (Thr) (covalent) #status predicted

Query Match 14.4%; Score 158.5; DB 1; Length 2415;
Best Local Similarity 29.1%; Pred. No. 1.8e-05;
Matches 52; Conservative 22; Mismatches 62; Indels 43; Gaps 11;
QY 6 QPVCRRGG---TORPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSISEDEQKLIKFI 62
Db 2202 QEVCEEKWNKYQCHCYR--HFPD---RETWVDAERRCREQSHLSSIVTPEEQ----EFV 2252
QY 63 ENLLPSDQDF-WIGLRRRREKQSNSTACQDLYAWTDGSIQFNNWYVDEPS---CGSEVC 118
Db 2253 NN---NAQDYQWIGL-----NDRTIEGDFRWSGDGHPMQFENWRPNQPDNFFAAGDC 2301
QY 119 VVM-YHQSPAPAGIGGYPYMFQWDDRCNMKNFICKYS----DEKPAVPSREAEGEETE 172
Db 2302 VVMIWHEKG-----EWNDVPCNYHLPTCKKGTVACGEPVVEHARTFGQKXD 2349

RESULT 14
B42755
E-selectin precursor - mouse
N;Alternate names: endothelial leukocyte adhesion molecule 1 (ELAM-1)
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 31-Dec-2000 #text_change 02-Aug-2002
C;Accession: S23174; B42755
R;Becker-Andre, M.; van Huijsduijnen, R.H.; Losberger, C.; Whelan, J.; Delamarter, J.F.
Eur. J. Biochem. 206, 401-411, 1992
A;Title: Murine endothelial leukocyte-adhesion molecule 1 is a close structural and funct
A;Reference number: S23174; MUID:92283265; PMID:1375914
A;Accession: S23174
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-612 <BEC>
A;Cross-references: GB:M80778; NID:g193014; PIDN:AAA37547.1; PID:g193015
R;Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A;Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-selectin
A;Reference number: A42755; MUID:92340571; PMID:1378846
A;Accession: B42755
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 'MKTAGV',1-389,391-612 <WEL>
A;Cross-references: GB:M87862; NID:g193107
A;Experimental source: endothelial cells
A;Note: sequence extracted from NCBI backbone (NCBI:109470)
A;Note: the sequence in GenBank entry MUSESELEC, release 117.0, (PIDN:AAA37577.1; PID:g19
A;Note: it is uncertain whether the initiator is Met-1 or the AUG codon preceding that
C;Superfamily: P-selectin; C-type lectin homology; complement factor H repeat homology; E
C;Keywords: glycoprotein; transmembrane protein

F;1-21/Domain: signal sequence #status predicted <SIG>
F;12-138/Domain: C-type lectin homology <LCH>
F;22-612/Product: p-selectin #status predicted <MAT>
F;143-174/Domain: EGF homology <EGF>
F;180-238/Domain: complement factor H repeat homology <FH1>
F;243-300/Domain: complement factor H repeat homology <FH2>
F;305-363/Domain: complement factor H repeat homology <FH3>
F;368-426/Domain: complement factor H repeat homology <FH4>
F;431-489/Domain: complement factor H repeat homology <FH5>
F;494-548/Domain: complement factor H repeat homology <FH6>
F;25,391,528/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.0%; Score 154.5; DB 2; Length 612;
Best Local Similarity 27.9%; Pred. No. 8.3e-06;
Matches 38; Conservative 28; Mismatches 45; Indels 25; Gaps 5;

QY 22 YFHDTSRRLNFEEAKEACRRDGGQLVSISEDEQKLIKFIENLLPSDGDGFWIGLRRREE 81
|:::| : : : : : |:::| : : : : : |:::| : : : : : |:::| : : : : :
Db 23 YYNASSELMTYDEASAYCQRDYTHLVAIQNKEE---INYLNSNLKHSPSYWIGIRK--- 76
|:::| : : : : : |:::| : : : : : |:::| : : : : : |:::| : : : : :
QY 82 KQSNSTACQDLVAVTDGS---ISQFRNWTYVDEPS---CGSEVCVMYHQPSAPAGIGGPPYM 136
|:::| : : : : : |:::| : : : : : |:::| : : : : : |:::| : : : : :
Db 77 -----VNNVWIVVGTGKPLTEEAQNWAPGEPNNKQRNEDCVEIYIQTKDSGM----- 124
|:::| : : : : : |:::| : : : : : |:::| : : : : : |:::| : : : : :
QY 137 FQWDDRCNMKNNFIC 152
|:::| : : : : : |:::| : : : : : |:::| : : : : : |:::| : : : : :
Db 125 --WDERCNKKLALC 138
|:::| : : : : : |:::| : : : : : |:::| : : : : : |:::| : : : : :
RESULT 15
A28452
proteoglycan core protein precursor, cartilage - rat
N;Alternate names: aggrecan
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 21-Jan-2000
C;Accession: A92623; A23835; A28453; A28095; A28452
R;Dooge, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 262, 17757-17767, 1987
A;Title: Complete primary structure of the rat cartilage proteoglycan core protein deduced from complementary DNA sequence
A;Reference number: A92623; MUID:88087070; PMID:3693370
A;Accession: A92623
A;Molecule type: mRNA
A;Residues: 1-2124 <DOE>
R;Dooge, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 263, 10040a, 1988
A;Reference number: A30069
A;Contents: annotation; revision to residue 698
R;Dooge, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 261, 8108-8111, 1986
A;Title: Partial cDNA sequence encoding a globular domain at the C terminus of the rat core protein
A;Reference number: A23835; MUID:86250698; PMID:2424893
A;Accession: A23835
A;Molecule type: mRNA
A;Residues: 1856-2124 <DO2>
A;Cross-references: GB:M13518; NID:g206104; PIDN:AAA41836.1; PID:g206105
R;Neame, P.J.; Christner, J.E.; Baker, J.R.
J. Biol. Chem. 262, 17768-17778, 1987
A;Title: Cartilage proteoglycan aggregates. The link protein and proteoglycan amino-terminal domain
A;Reference number: A28453; MUID:88087071; PMID:3693371
A;Accession: A28453
A;Molecule type: protein
A;Residues: 20-37, 'W', 39-60, 'E', 62-64, 'X', 66-69; 70-83; 84, 89-148, 'L', 150-238, 'S', 240, 'A', 242, 'G', 244, 'D', 246, 'E', 248, 'K', 250, 'R', 252, 'Q', 254, 'N', 256, 'I', 258, 'L', 260, 'K', 262, 'R', 264, 'Q', 266, 'N', 268, 'I', 270, 'K', 272, 'R', 274, 'Q', 276, 'N', 278, 'I', 280, 'K', 282, 'R', 284, 'Q', 286, 'N', 288, 'I', 290, 'K', 292, 'R', 294, 'Q', 296, 'N', 298, 'I', 300, 'K', 302, 'R', 304, 'Q', 306, 'N', 308, 'I', 310, 'K', 312, 'R', 314, 'Q', 316, 'N', 318, 'I', 320, 'K', 322, 'R', 324, 'Q', 326, 'N', 328, 'I', 330, 'K', 332, 'R', 334, 'Q', 336, 'N', 338, 'I', 340, 'K', 342, 'R', 344, 'Q', 346, 'N', 348, 'I', 350, 'K', 352, 'R', 354, 'Q', 356, 'N', 358, 'I', 360, 'K', 362, 'R', 364, 'Q', 366, 'N', 368, 'I', 370, 'K', 372, 'R', 374, 'Q', 376, 'N', 378, 'I', 380, 'K', 382, 'R', 384, 'Q', 386, 'N', 388, 'I', 390, 'K', 392, 'R', 394, 'Q', 396, 'N', 398, 'I', 400, 'K', 402, 'R', 404, 'Q', 406, 'N', 408, 'I', 410, 'K', 412, 'R', 414, 'Q', 416, 'N', 418, 'I', 420, 'K', 422, 'R', 424, 'Q', 426, 'N', 428, 'I', 430, 'K', 432, 'R', 434, 'Q', 436, 'N', 438, 'I', 440, 'K', 442, 'R', 444, 'Q', 446, 'N', 448, 'I', 450, 'K', 452, 'R', 454, 'Q', 456, 'N', 458, 'I', 460, 'K', 462, 'R', 464, 'Q', 466, 'N', 468, 'I', 470, 'K', 472, 'R', 474, 'Q', 476, 'N', 478, 'I', 480, 'K', 482, 'R', 484, 'Q', 486, 'N', 488, 'I', 490, 'K', 492, 'R', 494, 'Q', 496, 'N', 498, 'I', 500, 'K', 502, 'R', 504, 'Q', 506, 'N', 508, 'I', 510, 'K', 512, 'R', 514, 'Q', 516, 'N', 518, 'I', 520, 'K', 522, 'R', 524, 'Q', 526, 'N', 528, 'I', 530, 'K', 532, 'R', 534, 'Q', 536, 'N', 538, 'I', 540, 'K', 542, 'R', 544, 'Q', 546, 'N', 548, 'I', 550, 'K', 552, 'R', 554, 'Q', 556, 'N', 558, 'I', 560, 'K', 562, 'R', 564, 'Q', 566, 'N', 568, 'I', 570, 'K', 572, 'R', 574, 'Q', 576, 'N', 578, 'I', 580, 'K', 582, 'R', 584, 'Q', 586, 'N', 588, 'I', 590, 'K', 592, 'R', 594, 'Q', 596, 'N', 598, 'I', 600, 'K', 602, 'R', 604, 'Q', 606, 'N', 608, 'I', 610, 'K', 612, 'R', 614, 'Q', 616, 'N', 618, 'I', 620, 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A;Experimental source: clone T04A8

C;Genetics:

A;Gene: CESP:T04A8.3

A;Map position: 3

A;Introns: 25/2; 43/2; 130/1; 272/1; 326/1

Query Match 13.6%; Score 149.5; DB 2; Length 459;

Best Local Similarity 28.5%; Pred. No. 1.6e-05;

Matches 49; Conservative 23; Mismatches 52; Indels 48; Gaps 9;

QY 17 CYKVIYFHTSRRLNFEEAKEACRRDGGQLVSEDEQKLEKFIENLLPSDGF--WI 74

Db 287 CHK--YVHDM--MNDDAEKKNMGALSSFTTYEELKLLDEMILEVYPNDNNIAVWL 342

QY 75 GLRREKQSNSTACQDL-----YAWTDGSIQ-----FR 104

Db 343 GAXRREE-----CGDLSKNFTGGYSKDIHDPCARSRVFEWQNG-VAQNPPIFVGDGFD 394

QY 105 NW---YVDEPSCGSEVCW-MYHQPSAPAGIGGYPYMFQWDDRCNMKNFIC 152

Db 395 YWAEKYEPNHSSTDSERCLVQMSGMSVWYGDKNPRNMQINDIYCNIEFKFLC 446

RESULT 18

LNHUE

IgE Fc receptor II, low-affinity [validated] - human

N;Alternate names: Blast-2; CD23; Fc-epsilon-R11; lymphocyte IgE receptor

N;Contains: IgE Fc receptor II, splice form a; IgE Fc receptor II, splice form a'; IgE F

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 15-Sep-2000

C;Accession: A26067; S03279; S39442; S39443; A26164; A26589; A31924; J10132; S29107

R;Kikutani, H.; Inui, S.; Sato, R.; Barsumian, E.L.; Owaki, H.; Yamasaki, K.; Kaisho, T.

Cell 47, 657-665, 1986

A;Title: Molecular structure of human lymphocyte receptor for immunoglobulin E.

A;Reference number: A26067; MUID:87051737; PMID:2877743

A;Accession: A26067

A;Molecule type: mRNA

A;Residues: 1-321 <KIK>

A;Cross-references: GB:M14766; NID:G182449; PIDN:AAA52435.1; PID:G182450

A;Experimental source: EBV-transformed B lymphoblastoid cells RPMI-8856

R;Suter, U.; Bastos, R.; Hofstetter, H.

Nucleic Acids Res. 15, 7295-7308, 1987

A;Title: Molecular structure of the gene and the 5'-flanking region of the human lympho

A;Reference number: S03279; MUID:88015596; PMID:2958779

A;Accession: S03279

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 157-284 <SUT>

A;Cross-references: GB:X06049; NID:G31316

A;Note: all exon sequences were determined but the complete sequence is not shown

R;Matsui, M.; Nunez, R.; Sachi, Y.; Lynch, R.G.; Yodoi, J.

FEBS Lett. 335, 51-56, 1993

A;Title: Alternative transcripts of the human CD23/Fc-epsilon-R11. A possible novel mech

A;Reference number: S39442; MUID:94063078; PMID:8243664

A;Accession: S39442

A;Molecule type: DNA

A;Residues: 1-7, 'D', 47-50 <MAS1>

A;Experimental source: splice form a'

A;Accession: S39443

A;Molecule type: DNA

A;Residues: 'MNPPSQ', 47-50 <MAS2>

A;Experimental source: splice form b'

R;Ludin, C.; Hofstetter, H.; Sarfati, M.; Levy, C.A.; Suter, U.; Alaimo, D.; Kilchherr,

EMBO J. 6, 109-114, 1987

A;Title: Cloning and expression of the cDNA coding for a human lymphocyte IgE receptor.

A;Reference number: A26164; MUID:87218454; PMID:3034567

A;Accession: A26164

A;Molecule type: mRNA

A;Residues: 1-268, 'T', 270-321 <LUD>

A;Cross-references: GB:X04772; NID:G34002; PIDN:CAA28465.1; PID:G34003

A;Note: the codon given for 269-Asn (ACC) is inconsistent with the authors' translation

A;Note: part of this sequence, including the amino end of soluble forms of the protein,

R;Ikuta, K.; Takami, M.; Kim, C.W.; Honjo, T.; Miyoshi, T.; Tagaya, Y.; Kawabe, T.; Yodo

Proc. Natl. Acad. Sci. U.S.A. 84, 819-823, 1987

A;Title: Human lymphocyte Fc receptor for IgE: sequence homology of its cloned cDNA with

A;Reference number: A26589; MUID:87118255; PMID:2949326

A;Accession: A26589

A;Molecule type: mRNA

A;Residues: 1-321 <IKU>

A;Cross-references: GB:M15059; NID:G182447; PIDN:AAA52434.1; PID:G182448

A;Note: part of this sequence, including the amino end of soluble forms of the protein,

R;Yokota, A.; Kikutani, H.; Tanaka, T.; Sato, R.; Barsumian, E.L.; Suemura, M.; Kishimoto

Cell 55, 611-618, 1988

A;Title: Two species of human Fc-epsilon receptor II (Fc-epsilon-R11/CD23): tissue-specifi

A;Reference number: A31924; MUID:89028672; PMID:2972386

A;Accession: A31924

A;Molecule type: mRNA

A;Residues: 'MNPPSQ', 8-14 <YOK>

A;Cross-references: GB:M23562; NID:G182444

A;Experimental source: splice form I1b

R;Letellier, M.; Sarfati, M.; Delespesse, G.

Mol. Immunol. 26, 1105-1112, 1989

A;Title: Mechanisms of formation of IgE-binding factors (soluble CD23)-I. Fc epsilon R 11

A;Reference number: J10132; MUID:90220658; PMID:2534424

A;Accession: J10132

A;Molecule type: protein

A;Residues: 1-321 <LET>

A;Experimental source: lymphoblastoid B cell line

R;Rose, K.; Turcatti, G.; Graber, P.; Pochon, S.; Regamey, P.O.; Jansen, K.U.; Magnenat,

Biochem. J. 286, 819-824, 1992

A;Title: Partial characterization of natural and recombinant human soluble CD23.

A;Reference number: S29107; MUID:93038513; PMID:1417742

A;Accession: S29107

A;Molecule type: protein

A;Residues: 152-166; 173-179; 189-212; 230-263; 268-306 <ROS>

R;Padlan, E.A.; Helm, B.A.

submitted to the Brookhaven Protein Data Bank, June 1993

A;Reference number: A51791; PDB:1HLI

A;Contents: annotation; conformation by theoretical model, residues 173-285

R;Bajorath, J.

submitted to the Brookhaven Protein Data Bank, November 1995

A;Reference number: A65963; PDB:1KJE

A;Contents: annotation; conformation by theoretical model, residues 173-285

C;Comment: The sequence of the splice form a is shown.

C;Comment: This receptor for the Fc portion of IgE is expressed in various hematopoietic

ells.

C;Comment: Splice form a is expressed constitutively in B-cells; b is expressed in other

C;Comment: Soluble IgE-binding factors are produced by proteolytic cleavage of IgE Fc rec

C;Genetics:

A;Gene: GDB:FCER2; FCE2

A;Cross-references: GDB:118888; OMIM:151445

A;Map position: 19p13.3-19p13.3

A;Introns: 8/1; 46/1; 64/1; 85/1; 106/1; 127/1; 157/1; 157/3; 243/2

C;Superfamily: IgE receptor II; C-type lectin homology

C;Keywords: alternative splicing; B-cell; glycoprotein; immunoglobulin receptor; macropha

F; 'MNPPSQ', 47-321/Product: IgE Fc receptor II, splice form b' #status predicted <SFB1>

F; 'MNPPSQ', 8-321/Product: IgE Fc receptor II, splice form b' #status predicted <SFB>

F; 1-321/Product: IgE Fc receptor II, splice form a' #status predicted <SFA>

F; 1-231/Domain: intracellular #status predicted <INT>

F; 1-7, 'D', 47-321/Product: IgE Fc receptor II, splice form a' #status predicted <SFA1>

F; 14-20/Region: stop-transfer sequence

F; 22-45/Domain: transmembrane #status predicted <TMM>

F; 46-321/Domain: extracellular #status predicted <EXT>

F; 64-84/Region: 21-residue repeat

F; 81-321/Product: soluble IgE-binding factor (37K) #status predicted <IGE>

F; 85-105/Region: 21-residue repeat

F; 102-321/Product: soluble IgE-binding factor (33K) #status predicted <IGB>

F; 106-126/Region: 21-residue repeat

F; 125-321/Product: soluble IgE-binding factor (29K) #status predicted <IGI>

F; 148-321/Product: soluble IgE-binding factor (25-27K), long form #status experimental <

F; 150-321/Product: soluble IgE-binding factor (25-27K), short form #status experimental <

F; 163-282/Domain: C-type lectin homology <LCH>

F; 63/Binding site: carbohydrate (Asn) (covalent) #status predicted

F; 147-148/Cleavage site: Lys-Leu (unidentified proteinase) #status experimental

F; 149-150/Cleavage site: Arg-Met (unidentified proteinase) #status experimental

F; 191-282,259-273/Disulfide bonds: #status experimental

Query Match 13.5%; Score 149; DB 1; Length 321;
Best Local Similarity 30.2%; Pred. No. 1.2e-05;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;
QY 14 QRPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSISEDEQKLIIEFIENLLPSDGDWF 73
Db 171 QRKCY---YFGKGTQ--WVHARYACDDMEGQLVSIHSPEEQDFTKH-----ASHTGSW 220
QY 74 IGLRRREKQSNSTACQDLYAWTDGSGISQFRNMYVDEPSCGS--EVCVVMYHQPSAPAGI 131
Db 221 IGLRNLDLKE-----FIWVDGSHVDYSNAPGEPSTRSQGEDCVMM-----RGS 265
QY 132 GGPYMFQWDDRCNMK--NNPICKYSDEKPAV---PSREAEGE-----ETELTTPV 177
Db 266 G-----RWNDAFCDRKLGAWVC---DRLATCTPPASEGSAESMGPSRPPDPGRLPTPS 316
QY 178 LP 179
Db 317 AP 318
RESULT 19
T46256
brevican - human (fragment)
N;Alternate names: protein DKFZp761L191.1
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
C;Accession: T46256
R;Ottenwaeider, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23031
A;Accession: T46256
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-330 <AAA>
A;Cross-references: EMBL:AL137504
A;Experimental source: adult amygdala; clone DKFZp761L191
C;Genetics:
A;Note: DKFZp761L191.1
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EQ
Query Match 13.5%; Score 148.5; DB 2; Length 330;
Best Local Similarity 29.5%; Pred. No. 1.4e-05;
Matches 46; Conservative 16; Mismatches 57; Indels 37; Gaps 8;
QY 5 GQPVCRGG---TQRPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSISEDEQKLIIEF 61
Db 103 GLRFCNPGWDAFGQACYK---HFSTR-SWEAEFTQCRMYGAHLASISPEEQDFINR 157
QY 62 IENLLPSDGDGFWIGLRRREKQSNSTACQDLYAWTDGSGISQFRNMYVDEPS---CGSEVC 118
Db 158 YREYQ-----WIGL-----NDRTIEGDFLWSDGVPLLYENWNPQDPSYFLSGENC 203
QY 119 VVM-YHQPSAPAGIGGPPYMFQWDDRCNMKNFICK 153
Db 204 VVMVWHDQG-----QWSDVPCNYHLSYICK 228
RESULT 20
E89130
protein F52E1.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E89130
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: E89130
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-253 <STO>
A;Cross-references: GB:chr_V; PIDN:AAB37037.1; PID:g1086809; GSPDB:GN00023; CESP:F52E1.2
C;Genetics:
A;Gene: F52E1.2
A;Map position: 5
Query Match 13.5%; Score 148; DB 2; Length 253;
Best Local Similarity 29.2%; Pred. No. 1.1e-05;
Matches 49; Conservative 24; Mismatches 57; Indels 38; Gaps 10;
QY 9 CRGG-----TQRPCYKV-IYFHDTSRRLNFE-----AKEACRRDGGQLVSIIES 51
Db 96 CPGCPTGWQYLNNSKCYKVLHFHCLSLKVQLQKFDAAVTVYAGATSACAAQGAELVTIDS 155
QY 52 EDEQKLIIEFIEN--LLPSDGDGFWIGLRRREKQSNSTACQDLYAWTDGSGISQFRNMYVD 109
Db 156 FDENDALRKAFDTNALVDETKETWIGLK-----SLSGAWQ---WADGSSATYTNWAPS 205
QY 110 EPSCGSEVCVVMYHQPSAPAGIGGPPYMFQ---WNDDRCNMKN-NFICK 153
Db 206 QPS-SNGLCVQMITSLSNA-----TYKYQGGWKTYGCGKTSASYICE 248
RESULT 21
A55182
aggrecan precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: A55182; S55329; S50207; S51355; I78532; I58123
R;Walcz, E.; Deak, F.; Erhardt, P.; Coulter, S.N.; Fueloep, C.; Horvath, P.; Doege, K.J.
Genomics 22, 364-371, 1994
A;Title: Complete coding sequence, deduced primary structure, chromosomal localization,
A;Reference number: A55182; MUID:95104847; PMID:7806222
A;Accession: A55182
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-2132 <WAL>
A;Cross-references: GB:L07049; NID:g678541; PIDN:AAC37670.1; PID:g191772
R;Watanabe, H.; Gao, L.; Sugiyama, S.; Doege, K.; Kimata, K.; Yamada, Y.
Biochem. J. 308, 433-440, 1995
A;Title: Mouse aggrecan, a large cartilage proteoglycan: protein sequence, gene structur
A;Reference number: S55329; MUID:95289972; PMID:7772024
A;Accession: S55329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-567,'G',569-1728,'I',1730-2132 <WAT1>
A;Cross-references: GB:U22901; NID:g886014
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Accession: S50207
A;Molecule type: mRNA
A;Residues: 350-481,'R',483-506 <GLU1>
A;Cross-references: EMBL:X80279; NID:g673432
R;Glumoff, V.
submitted to the EMBL Data Library, July 1994
A;Reference number: S51355
A;Accession: S51355
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 350-383,'CPVMSQRRPWA' <GLU2>
A;Cross-references: EMBL:X80279
R;Watanabe, H.; Kimata, K.; Line, S.; Strong, D.; Gao, L.Y.; Kozak, C.A.; Yamada, Y.
Nature Genet. 7, 154-157, 1994
A;Title: Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in the aggrec
A;Reference number: I58123; MUID:95004579; PMID:7920633
A;Accession: I78532
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 211-326 <WAT2>
A;Cross-references: GB:S73722; NID:g765215; PIDN:AAB32160.1; PID:g765216

A;Accession: I58123
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 211-240, 'MCTASLRWRVRSMRHPQRNPSRRQPTS', 'AGGWGHAWPPQASSTWPGRAVWTCALAGW', 'R
A;Cross-references: GB:S73720; NID:G765211; PIDN:AAB32159.1; PID:G765212
C;Genetics:
A;Map position: 7
A;Introns: 253/1
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: cartilage; extracellular matrix
F;1-19/Domain: signal sequence #status predicted <SIG>
F;44-135/Domain: immunoglobulin homology <IMM>
F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;504-581/Domain: link protein repeat homology <LNK3>
F;602-683/Domain: link protein repeat homology <LNK4>
F;1922-2042/Domain: C-type lectin homology <LCH>
F;2049-2105/Domain: complement factor H repeat homology <FHD>

Query Match 13.4%; Score 147.5; DB 1; Length 2132;
Best Local Similarity 24.7%; Pred. No. 0.00015;
Matches 45; Conservative 30; Mismatches 64; Indels 43; Gaps 9;

QY 3 LSGQPVCRRG---TQRPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSI ESEDEQKLI E 59
Db 1916 VADQECCCEGWTKFQGHCHYR--HFPPD---RETWVDAERRCQSHLSIVTPEEQEFVN 1970

QY 60 KFIENLLPSDGF-WIGLRRREKQSNSTACQDLYAWTDGSI SFRNMYVDEP---SCG 114
Db 1971 KNAQ-----DYQWIGL-----NDRTEGDFRWSGDGHSLOPEKWRPNQDNFFATG 2015

QY 115 SEVCVMYHQSPAPAGIGPYPMFQWNDRCNMKNFICKYS----DEKPAVPSREAE GEE 170
Db 2016 EDCVVMWHERG-----EWNDVPCNYQLPFTCKGTACGDPFVVEHARTLGQK 2064

QY 171 TE 172
Db 2065 KD 2066

RESULT 22
S57653
brevican precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
C;Accession: S57653
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning and sequence of mouse neurocan and brevican and their different e
A;Reference number: S57653
A;Accession: S57653
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-883 <RAU>
A;Cross-references: EMBL:X87096; NID:G886889; PIDN:CAA60575.1; PID:G886890
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
F;49-138/Domain: immunoglobulin homology <IMM>
F;173-250/Domain: link protein repeat homology <LNK1>
F;271-352/Domain: link protein repeat homology <LNK2>
F;626-657/Domain: EGF homology <EGF>
F;664-784/Domain: C-type lectin homology <LCH>
F;791-847/Domain: complement factor H repeat homology <FHD>

Query Match 13.4%; Score 147; DB 2; Length 883;
Best Local Similarity 29.7%; Pred. No. 5.9e-05;
Matches 43; Conservative 21; Mismatches 45; Indels 36; Gaps 8;

QY 14 QRPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSI ESEDEQKLI -EKFIENLLPSDGF 72
Db 672 QGACYK---HFSTRR-SWEAEASQCRAALGAHLT SICTPEQDFVNDRYEQ----- 719
QY 73 WIGLRRREKQSNSTACQDLYAWTDGSI SFRNMYVDEPS---CGSEVCVM-YHQPSAP 128

Db 720 WIGL-----NDRTEGDFLWSGAPLLYENWNPQPD SYFLSCGNCVVMVWHDQG-- 769
QY 129 AGIGPYPMFQWNDRCNMKNFICK 153
Db 770 -----QWSDVPCNYHLSYTC 785

RESULT 23
LNRC1
lectin BRA3-1 precursor - barnacle (Megabalanus rosa)
C;Species: Megabalanus rosa
C;Date: 24-Feb-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: JCI503; A26094
R;Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, T.
Gene 128, 251-255, 1993
A;Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure and
A;Reference number: JCI503; MUID:93292994; PMID:8514190
A;Accession: JCI503
A;Molecule type: DNA; mRNA
A;Residues: 1-162 <TAK>
A;Cross-references: DDBJ:D13299
R;Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 874, 285-295, 1986
A;Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
A;Reference number: A26094
A;Accession: A26094
A;Molecule type: protein
A;Residues: 25-145, 'K', '147-162 <MUR>
A;Note: 146-Arg was also found
C;Comment: This galactose-binding lectin is isolated from the coelomic fluid.
C;Comment: This protein plays important roles in defense mechanisms and in development ar
C;Comment: The molecule is a tetramer of identical chains.
C;Genetics:
A;Introns: 22/1; 47/2; 86/3
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemolymph; homotetramer; lectin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-162/Product: lectin BRA3-1 #status experimental <MAT>
F;26-150/Domain: C-type lectin homology <LCH>
F;26-39, 56-150, 125-142/Disulfide bonds: #status experimental
F;157/Disulfide bonds: interchain (to 160) #status experimental
F;160/Disulfide bonds: interchain (to 157) #status experimental

Query Match 13.3%; Score 146.5; DB 1; Length 162;
Best Local Similarity 25.0%; Pred. No. 9.1e-06;
Matches 40; Conservative 26; Mismatches 59; Indels 35; Gaps 6;

QY 2 LLSGQPVCRRGSTRPCYKVIYFHDTSRRLNFEAKEACR--RDGQLVSI ESEDEQKLI E 59
Db 19 ITTGECTCPGNLDWQYDGHCHYASITVQVRWDAQLACQTVHPGAYLATIQSLENAFIS 78

QY 60 KFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSI SFRNMYVDEPS-----C 113
Db 79 ETVSN-----NRLWIGL-----NDIDLEGHYVWSNGEATFTYSSNNPNWENQDC 125

QY 114 GSEVCVMYHQSPAPAGIGPYPMFQWNDRCNMKNFICK 153
Db 126 G----VVNYDTVTG-----QWDDDDCNKRNFLCK 151

RESULT 24
I50421
aggrecan precursor - chicken
N;Alternate names: cartilage chondroitin sulfate proteoglycan core protein
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
C;Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072
R;Li, H.; Schwartz, N.B.; Vertel, B.M.
J. Biol. Chem. 268, 23504-23511, 1993
A;Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and
A;Reference number: A48884; MUID:94043149; PMID:8226878
A;Accession: I50421
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-2109 <LIX>
A;Cross-references: GB:L21913; NID:G416133; PIDN:AAB19128.1; PID:G416134
R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 296, 885-887, 1993
A;Reference number: S39796; MUID:94107258; PMID:8280087
A;Contents: annotation; erratum
A;Accession: S39796
A;Molecule type: mRNA
A;Residues: 1-361, 'DL', 364-600, 'R', 602-999, 'R', 1001-1028, 'P', 1030-1250, 'D', 1252-1602, 'A'
A;Cross-references: GB:M88101
R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 288, 903-910, 1992
A;Title: Molecular cloning of chicken aggrecan. Structural analyses.
A;Reference number: S27356; MUID:93111968; PMID:1339285
A;Accession: S27356
A;Molecule type: mRNA
A;Residues: 1-361, 'DL', 364-600, 'R', 602-999, 'R', 1001-1028, 'P', 1030-1250, 'D', 1252-1549, 'T'
A;Cross-references: EMBL:M88101
R;Sai, S.; Tanaka, T.; Koshier, R.A.; Tanzer, M.L.
Proc. Natl. Acad. Sci. U.S.A. 83, 5081-5085, 1986
A;Title: Cloning and sequence analysis of a partial cDNA for chicken cartilage proteogly
A;Reference number: A25442; MUID:86259736; PMID:3460082
A;Accession: A25442
A;Molecule type: mRNA
A;Residues: 1693-1795, 'G', 1797-1855, 1894-2109 <SAI>
A;Cross-references: GB:M13993; NID:G211654; PIDN:AAA48720.1; PID:G211655
A;Experimental source: sternal cartilage
R;Tanaka, T.; Har-El, R.; Tanzer, M.L.
J. Biol. Chem. 263, 15831-15835, 1988
A;Title: Partial structure of the gene for chicken cartilage proteoglycan core protein.
A;Reference number: A32002; MUID:89008500; PMID:3170613
A;Accession: A32002
A;Molecule type: DNA
A;Residues: 1893-1987, 'S', 1989-2022 <TAN>
A;Note: the authors translated the codon TCC for residue 1787 as Phe
R;Krueger, R.C.
J. Biol. Chem. 265, 12088-12097, 1990
A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide s
A;Reference number: I50216; MUID:90307744; PMID:1694853
A;Accession: I50216
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'PA', 1044-1559 <XRU>
A;Cross-references: GB:M38187; NID:G211685; PIDN:AAA48731.1; PID:G555441
R;Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.
J. Biol. Chem. 265, 12075-12087, 1990
A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation an
A;Reference number: A37072; MUID:90307743; PMID:2365711
A;Accession: A37072
A;Molecule type: protein
A;Residues: 998-1015, 'X', 1017-1019, 'X', 1021-1023 <KR2>
A;Note: amino end of 86K core peptide CS-A
A;Accession: B37072
A;Molecule type: protein
A;Residues: 1247-1250, 'D', 1252-1272, 'X', 1274-1275 <KR3>
A;Note: amino end of 75K core peptide CS-B
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: alternative splicing
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-2109/Product: aggrecan #status predicted <MAT>
F;44-131/Domain: immunoglobulin homology <IMM>
F;166-243/Domain: link protein repeat homology <LNK1>
F;264-346/Domain: link protein repeat homology <LNK2>
F;537-614/Domain: link protein repeat homology <LNK3>
F;635-716/Domain: link protein repeat homology <LNK4>
F;1859-1890/Domain: EGF homology <EGF>
F;1897-2017/Domain: C-type lectin homology <LCH>
F;2024-2080/Domain: complement factor H repeat homology <FHD>

Query Match 13.3%; Score 146; DB 1; Length 2109;
Best Local Similarity 25.0%; Pred. No. 0.0002;
Matches 42; Conservative 28; Mismatches 58; Indels 40; Gaps 8;

QY 14 QRPCYKVIYFHTSRLNFEAEACRRDGGQLVSIESTEDEQKLIKFLENLLPSDGF- 72
Db QHCYR--HFEE---RETWDAESRCRHOHLSSIIITPEEQEFVNSHAQ-----DYQ 1952
QY 73 WIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS-----CGSEVCVVMYHQPSAP 128
Db WIGLSDR-----AVENDFRWSDGHSLOFENWRPNQPDNFFFAGEDCVVMWHEQG-- 2002
QY 129 AGIGGPMYFMQWDDRCNMKNNFICKYS---DEKPAVPSREAEGETE 172
Db 2003 -----EWNDVPCNYHLPTCKKGTVACGDPVVENARTFGRKKD 2041

RESULT 25
JC7595

scavenger receptor with C-type lectin type I - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7595

R;Nakamura, K.; Funakoshi, H.; Miyamoto, K.; Tokunaga, F.; Nakamura, T.

Biochem. Biophys. Res. Commun. 280, 1028-1035, 2001

A;Title: Molecular cloning and functional characterization of a human scavenger receptor

A;Reference number: JC7595; MUID:21092718; PMID:1162630

A;Contents: Placenta

A;Accession: JC7595

A;Molecule type: mRNA

A;Residues: 1-742 <NAK>

A;Cross-references: DDBJ:AB038518

C;Comment: This receptor, a member of the scavenger receptor family, belonging to the ty
important role in host defense. It forms a timer and plays a role in recognizing infect

C;Genetics:

A;Gene: srcl-I

A;Map position: 18p11.32

C;Keywords: coiled coil; glycoprotein; transmembrane protein

F;1-39/Domain: cytosolic (amino-terminus) #status predicted <CYT>

F;16-19/Region: internalization signal YKRF

F;40-56/Domain: transmembrane #status predicted <TMM>

F;57-112/Domain: extracellular #status predicted <EXT>

F;113-335/Domain: coiled coil #status predicted <COC>

F;369-384/Region: serine/threonine-rich #status predicted

F;443-589/Domain: collagen-like #status predicted <COL>

F;607-732/Domain: C-type lectin/carbohydrate recognition domain #status predicted <CRD>

Query Match 13.2%; Score 145.5; DB 2; Length 742;
Best Local Similarity 28.7%; Pred. No. 6.5e-05;
Matches 39; Conservative 17; Mismatches 61; Indels 19; Gaps 5;

QY 22 YFHDTSRLNFEAEACRRDGGQLVSIESTEDEQKLIKFLENLLPSDGFWIGLRRREE 81

Db YYFVSVEKEI-FEDAKLFCEDKSSHLVFINTREEQQWIKK-----QMVGRESHWIGLTDSE 673

QY 82 KQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCVVMYHQPSAPAGIGGPMYFMQWND 141

Db 674 ENE-----WKWLDGTSPDYKNWKAGQPDNNGH-----GHGPGEDCA-GLIYAGQWND 719

QY 142 DRCNMKNNFICKYSDE 157

Db 720 QCEDVNNFICEKDRE 735

Search completed: September 9, 2004, 22:57:39
Job time : 25.9386 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 9, 2004, 22:56:51 ; Search time 90.2776 Seconds
(without alignments)
721.109 Million cell updates/sec

Title: US-09-887-855-2_COPY_25_227
Perfect score: 1100
Sequence: 1 RLLSGQPVCRGGTQPCYKV.....EEDAKKTFKESREAAALNLAY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1100	100.0	206	9 US-09-887-855-5	Sequence 5, Appli
2	1100	100.0	374	9 US-09-887-855-2	Sequence 2, Appli
3	1100	100.0	374	14 US-10-149-819-15	Sequence 15, Appl
4	1100	100.0	374	15 US-10-094-749-2090	Sequence 2090, Ap
5	1100	100.0	374	15 US-10-264-237-2579	Sequence 2579, Ap
6	1100	100.0	374	16 US-10-648-593-148	Sequence 148, App
7	1100	100.0	387	12 US-10-296-115-1311	Sequence 1311, Ap
8	1096	99.6	374	15 US-10-094-749-2142	Sequence 2142, Ap
9	1090	99.1	374	12 US-10-351-334-166	Sequence 166, App
10	1086	98.7	382	9 US-09-909-320-137	Sequence 137, App
11	1086	98.7	382	9 US-09-909-088B-137	Sequence 137, App
12	1086	98.7	382	9 US-09-905-291A-137	Sequence 137, App
13	1086	98.7	382	9 US-09-902-853-137	Sequence 137, App
14	1086	98.7	382	9 US-09-907-824-137	Sequence 137, App
15	1086	98.7	382	9 US-09-907-841-137	Sequence 137, App

16	1086	98.7	382	10 US-09-904-011-137	Sequence 137, App
17	1086	98.7	382	10 US-09-906-742-137	Sequence 137, App
18	1086	98.7	382	10 US-09-906-838-137	Sequence 137, App
19	1086	98.7	382	10 US-09-907-613-137	Sequence 137, App
20	1086	98.7	382	10 US-09-907-942-137	Sequence 137, App
21	1086	98.7	382	10 US-09-904-859-137	Sequence 137, App
22	1086	98.7	382	10 US-09-909-204-137	Sequence 137, App
23	1086	98.7	382	10 US-09-904-820-137	Sequence 137, App
24	1086	98.7	382	10 US-09-904-786-137	Sequence 137, App
25	1086	98.7	382	10 US-09-906-646-137	Sequence 137, App
26	1086	98.7	382	10 US-09-906-700-137	Sequence 137, App
27	1086	98.7	382	10 US-09-903-786-137	Sequence 137, App
28	1086	98.7	382	10 US-09-902-903-137	Sequence 137, App
29	1086	98.7	382	10 US-09-903-749A-137	Sequence 137, App
30	1086	98.7	382	10 US-09-904-119-137	Sequence 137, App
31	1086	98.7	382	10 US-09-904-956-137	Sequence 137, App
32	1086	98.7	382	10 US-09-902-736-137	Sequence 137, App
33	1086	98.7	382	10 US-09-907-794-137	Sequence 137, App
34	1086	98.7	382	10 US-09-903-943-137	Sequence 137, App
35	1086	98.7	382	10 US-09-904-462-137	Sequence 137, App
36	1086	98.7	382	10 US-09-907-925-137	Sequence 137, App
37	1086	98.7	382	10 US-09-902-692-137	Sequence 137, App
38	1086	98.7	382	10 US-09-903-520-137	Sequence 137, App
39	1086	98.7	382	10 US-09-905-056-137	Sequence 137, App
40	1086	98.7	382	10 US-09-909-064-137	Sequence 137, App
41	1086	98.7	382	10 US-09-904-553-137	Sequence 137, App
42	1086	98.7	382	10 US-09-905-381-137	Sequence 137, App
43	1086	98.7	382	10 US-09-905-088-137	Sequence 137, App
44	1086	98.7	382	10 US-09-907-575-137	Sequence 137, App
45	1086	98.7	382	10 US-09-905-075-137	Sequence 137, App

ALIGNMENTS

RESULT 1
US-09-887-855-5
; Sequence 5, Application US/09887855
; Patent No. US20020058310A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Anderson, Dirk M
; TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES
; FILE REFERENCE: 2883-US
; CURRENT APPLICATION NUMBER: US/09/887,855
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-855-5

Query Match 100.0%; Score 1100; DB 9; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-103;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	RLLSGQPVCRGGTQPCYKVIYFHTSRLNFEEAKEACRRDGGQLVSI	EDEQKLIK	60
Db	4	RLLSGQPVCRGGTQPCYKVIYFHTSRLNFEEAKEACRRDGGQLVSI	EDEQKLIK	63
QY	61	FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSI	SQFNWYVDEPSCGSEVCV	120
Db	64	FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSI	SQFNWYVDEPSCGSEVCV	123
QY	121	MYHQSAPACIGGPFYMFQWNNDRCNMKNFNICKYSDEKPAVPSREAE	GEETELTTPVLPE	180
Db	124	MYHQSAPACIGGPFYMFQWNNDRCNMKNFNICKYSDEKPAVPSREAE	GEETELTTPVLPE	183
QY	181	ETQEEDAKKTFKESREAAALNLAY	203	
Db	184	ETQEEDAKKTFKESREAAALNLAY	206	

RESULT 2
US-09-887-855-2
; Sequence 2, Application US/09887855
; Patent No. US20020058310A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Anderson, Dirk M
; TITLE OF INVENTION: LECTIN SS3939 DNA AND POLYPEPTIDES
; FILE REFERENCE: 2883-US
; CURRENT APPLICATION NUMBER: US/09/887,855
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-855-2

Query Match 100.0%; Score 1100; DB 9; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.4e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLSGQPVCRGGTQRCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIIESEDEQKLIK 60
Db |||||
25 RLLSGQPVCRGGTQRCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIIESEDEQKLIK 84

Qy 61 FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCVV 120
Db |||||
85 FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCVV 144

Qy 121 MYHQPSAPAGIGGYPYFQWNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db |||||
145 MYHQPSAPAGIGGYPYFQWNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204

Qy 181 ETQEEDAKKTFKESREAAALNLAY 203
Db |||||
205 ETQEEDAKKTFKESREAAALNLAY 227

RESULT 3
US-10-149-819-15
; Sequence 15, Application US/10149819
; Publication No. US20030044913A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: SHAH, Purvi
; APPLICANT: LAL, Preeti
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PF-0760 PCT
; CURRENT APPLICATION NUMBER: US/10/149,819
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
; PRIOR FILING DATE: 1999-12-10; 1999-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030044913A1 3143411CD1

US-10-149-819-15

Query Match 100.0%; Score 1100; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.4e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLSGQPVCRGGTQRCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIIESEDEQKLIK 60
Db |||||
25 RLLSGQPVCRGGTQRCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIIESEDEQKLIK 84

Qy 61 FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCVV 120
Db |||||
85 FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCVV 144

Qy 121 MYHQPSAPAGIGGYPYFQWNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db |||||
145 MYHQPSAPAGIGGYPYFQWNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204

Qy 181 ETQEEDAKKTFKESREAAALNLAY 203
Db |||||
205 ETQEEDAKKTFKESREAAALNLAY 227

RESULT 4
US-10-094-749-2090
; Sequence 2090, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2090
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2090

Query Match 100.0%; Score 1100; DB 15; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.4e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLSGQPVCRGGTQRCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIIESEDEQKLIK 60
Db |||||
25 RLLSGQPVCRGGTQRCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIIESEDEQKLIK 84

Qy 61 FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCVV 120
Db |||||
85 FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCVV 144

QY 121 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204
QY 181 ETQEEADAKKTFKESREAAINLAY 203
Db 205 ETQEEADAKKTFKESREAAINLAY 227

RESULT 5
US-10-264-237-2579
; Sequence 2579, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2579
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2579

Query Match 100.0%; Score 1100; DB 15; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.4e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRCGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSISEDEQKLIK 60
Db 25 RLLSGQPVCRCGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSISEDEQKLIK 84

QY 61 FIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
Db 85 FIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 144

QY 121 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204

QY 181 ETQEEADAKKTFKESREAAINLAY 203
Db 205 ETQEEADAKKTFKESREAAINLAY 227

RESULT 6
US-10-648-593-148
; Sequence 148, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-648-593-148

Query Match 100.0%; Score 1100; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.4e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRCGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSISEDEQKLIK 60
Db 25 RLLSGQPVCRCGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSISEDEQKLIK 84

QY 61 FIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
Db 85 FIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 144

QY 121 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204

QY 181 ETQEEADAKKTFKESREAAINLAY 203
Db 205 ETQEEADAKKTFKESREAAINLAY 227

RESULT 7
US-10-296-115-1311
; Sequence 1311, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1311
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1311

Query Match 100.0%; Score 1100; DB 12; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.5e-102;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRCGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSISEDEQKLIK 60
Db 38 RLLSGQPVCRCGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSISEDEQKLIK 97

QY 61 FIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
Db 98 FIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 157

QY 121 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 158 MYHQPAPAGIGGPFQWQNDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 217

QY 181 ETQEEADAKKTFKESREAAINLAY 203
Db 218 ETQEEADAKKTFKESREAAINLAY 240

RESULT 8
US-10-094-749-2142
; Sequence 2142, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI

APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2142
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2142

Query Match 99.6%; Score 1096; DB 15; Length 374;
Best Local Similarity 99.5%; Pred. No. 3.6e-102;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSI ESEDEQKLI EK 60
Db 25 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSI ESEDEQKLI EK 84

QY 61 FIENLLPSDGDGFWIGLRRRREKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGSEVCV 120
Db 85 FIENLLPSDGDGFWIGLRRRREKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGSEVCV 144

QY 121 MYHQSPAPAGIGGPFYMFQWDDRCNMKNFNICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHQSPAPAGIGGPFYMFQWDDRCNMKNFNICKYSDEKPAVPSREAEGETELTTPVLPE 204

QY 181 ETQEDAKKTFKESREAAALNLAY 203
Db 205 ETQEDAKKTFKESREAAALNLAY 227

RESULT 9
US-10-351-334-166
Sequence 166, Application US/10351334
Publication No. US20040034196A1
GENERAL INFORMATION:
APPLICANT: Komatsoulis et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P2
CURRENT APPLICATION NUMBER: US/10/351,334
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/350,898
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: 09/489,847
PRIOR FILING DATE: 2000-01-24
PRIOR APPLICATION NUMBER: PCT/US99/17130
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 60/094,657
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: 60/095,486
PRIOR FILING DATE: 1998-08-05
PRIOR APPLICATION NUMBER: 60/096,319

PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: 60/095,454
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 60/095,455
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 166
LENGTH: 374
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (84)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (112)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-351-334-166

Query Match 99.1%; Score 1090; DB 12; Length 374;
Best Local Similarity 99.0%; Pred. No. 1.4e-101;
Matches 201; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSI ESEDEQKLI EK 60
Db 25 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSI ESEDEQKLI EK 84

QY 61 FIENLLPSDGDGFWIGLRRRREKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGSEVCV 120
Db 85 FIENLLPSDGDGFWIGLRRRREKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGSEVCV 144

QY 121 MYHQSPAPAGIGGPFYMFQWDDRCNMKNFNICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHQSPAPAGIGGPFYMFQWDDRCNMKNFNICKYSDEKPAVPSREAEGETELTTPVLPE 204

QY 181 ETQEDAKKTFKESREAAALNLAY 203
Db 205 ETQEDAKKTFKESREAAALNLAY 227

RESULT 10
US-09-909-320-137
Sequence 137, Application US/09909320
Patent No. US20020132240A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

```

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-320-137

Query Match      98.7%; Score 1086; DB 9; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY      1  RLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFFEEAKEACRRDGGQLVSIESE 52
      |||
Db      25  RLLSASDLRLRGQPCVCRGGTQPCYKVIYFHDTSRRLNFFEEAKEACRRDGGQLVSIESE 84

QY      53  DEQKLEKFIENLLPSDGDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
      |||
Db      85  DEQKLEKFIENLLPSDGDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144

QY      113 CGSEVCVMYHQPSAPAGIGGPPYMFQWDDRCNMKNNFICKYSDEKPAVPSREAEGETE 172
      |||
Db      145 CGSEVCVMYHQPSAPAGIGGPPYMFQWDDRCNMKNNFICKYSDEKPAVPSREAEGETE 204

QY      173 LTPVLPEETQEDAKKTFKESREAAALNLAY 203
      |||
Db      205 LTPVLPEETQEDAKKTFKESREAAALNLAY 235

RESULT 11
US-09-909-088B-137
; Sequence 137, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
```

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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-088B-137
```

```

Query Match      98.7%; Score 1086; DB 9; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
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QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEAEAKEACRRDGGQLVSI ESE 52
| | | | |
Db 25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRRLNFEAEAKEACRRDGGQLVSI ESE 84
| | | | |
QY 53 DEQKLIKFIENLLPSDGDWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWNVDEPS 112
| | | | |
Db 85 DEQKLIKFIENLLPSDGDWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWNVDEPS 144
| | | | |
QY 113 CGSEVCVMYHQPSAPAGIGGYPYMFQWDDRCNMKNFNICKYSDEKPAVPSREAEGETE 172
| | | | |
Db 145 CGSEVCVMYHQPSAPAGIGGYPYMFQWDDRCNMKNFNICKYSDEKPAVPSREAEGETE 204
| | | | |
QY 173 LTTPLPEETQEDAKTKFKESREAAALNLAY 203
| | | | |
Db 205 LTTPLPEETQEDAKTKFKESREAAALNLAY 235
| | | | |

RESULT 12
US-09-905-291A-137
; Sequence 137, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens.
US-09-905-291A-137

Query Match 98.7%; Score 1086; DB 9; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEAEAKEACRRDGGQLVSI ESE 52
| | | | |
Db 25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRRLNFEAEAKEACRRDGGQLVSI ESE 84
| | | | |
QY 53 DEQKLIKFIENLLPSDGDWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWNVDEPS 112
| | | | |
Db 85 DEQKLIKFIENLLPSDGDWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWNVDEPS 144
| | | | |
QY 113 CGSEVCVMYHQPSAPAGIGGYPYMFQWDDRCNMKNFNICKYSDEKPAVPSREAEGETE 172
| | | | |
Db 145 CGSEVCVMYHQPSAPAGIGGYPYMFQWDDRCNMKNFNICKYSDEKPAVPSREAEGETE 204
| | | | |
QY 173 LTTPLPEETQEDAKTKFKESREAAALNLAY 203
| | | | |
Db 205 LTTPLPEETQEDAKTKFKESREAAALNLAY 235
| | | | |

RESULT 13
US-09-902-853-137
; Sequence 137, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-853-137

Query Match
Best Local Similarity 98.7%; Score 1086; DB 9; Length 382;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHTSRLNFEEAKEACRRDGGQLVSIESE 52
Db 25 RLLSASDLRLGGQPVCRGGTQPCYKVIYFHTSRLNFEEAKEACRRDGGQLVSIESE 84
QY 53 DEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
Db 85 DEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144
QY 113 CGSEVCVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGEETE 172
Db 145 CGSEVCVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGEETE 204
QY 173 LTPVLPEETQEEADAKTKFKESREAALNLAY 203
Db 205 LTPVLPEETQEEADAKTKFKESREAALNLAY 235

RESULT 14
US-09-907-824-137
Sequence 137, Application US/09907824
Publication No. US20020197671A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 137
LENGTH: 382
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-824-137

Query Match
Best Local Similarity 98.7%; Score 1086; DB 9; Length 382;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVPCRGGTQPCYKVIYFHDTSRRLNFFEEAKEACRRDGGQLVSIIESE 52
Db 25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRRLNFFEEAKEACRRDGGQLVSIIESE 84
QY 53 DEQKLEKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIISQFRNWWYVDEPS 112
Db 85 DEQKLEKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIISQFRNWWYVDEPS 144
QY 113 CGSEVCVMYHQPSAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 172
Db 145 CGSEVCVMYHQPSAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 204
QY 173 LTTPLPEETQEDAKKTFKESREAAALNLAY 203
Db 205 LTTPLPEETQEDAKKTFKESREAAALNLAY 235

RESULT 15

US-09-907-841-137
; Sequence 137, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-841-137
Query Match 98.7%; Score 1086; DB 9; Length 382;
Best local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 RLLS-----GQVPCRGGTQPCYKVIYFHDTSRRLNFFEEAKEACRRDGGQLVSIIESE 52
Db 25 RLLSASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRRLNFFEEAKEACRRDGGQLVSIIESE 84
QY 53 DEQKLEKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIISQFRNWWYVDEPS 112
Db 85 DEQKLEKFIENLLPSDGFWIGLRRREKQSNSTACQDLYAWTDGSIISQFRNWWYVDEPS 144
QY 113 CGSEVCVMYHQPSAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 172
Db 145 CGSEVCVMYHQPSAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 204
QY 173 LTTPLPEETQEDAKKTFKESREAAALNLAY 203
Db 205 LTTPLPEETQEDAKKTFKESREAAALNLAY 235

RESULT 16

US-09-904-011-137
; Sequence 137, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222

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; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-137

Query Match      98.7%;  Score 1086;  DB 10;  Length 382;
Best Local Similarity 96.2%;  Pred. No. 3.8e-101;
Matches 203;  Conservative 0;  Mismatches 0;  Indels 8;  Gaps 1;

QY      1  RLLS-----GQPVCRGGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
      |||||
Db      25  RLLSASDLDLRGQPVCRGGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 84

QY      53  DEQKLIKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
      |||||
Db      85  DEQKLIKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144

QY      113  CGSEVCVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGEETE 172
      |||||
Db      145  CGSEVCVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGEETE 204

QY      173  LTPVLPEETQEEDAKKTFKESREAALNLAY 203
      |||||
Db      205  LTPVLPEETQEEDAKKTFKESREAALNLAY 235

RESULT 17
US-09-906-742-137
; Sequence 137, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.

```

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; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-137

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Query Match      98.7%;  Score 1086;  DB 10;  Length 382;
Best Local Similarity 96.2%;  Pred. No. 3.8e-101;
Matches 203;  Conservative 0;  Mismatches 0;  Indels 8;  Gaps 1;

QY      1  RLLS-----GQPVCRGGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
      |||||
Db      25  RLLSASDLDLRGQPVCRGGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 84

QY      53  DEQKLIKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
      |||||
Db      85  DEQKLIKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144

QY      113  CGSEVCVMYHQPSAPAGIGGPPYMFQWNDRCNMKNFICKYSDEKPAVPSREAEGEETE 172

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Db 145 CGSEVCMVYHQPSPAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 204
QY 173 LTTVPVLPETQEDAKTKFKESREAAALNLAY 203
Db 205 LTTVPVLPETQEDAKTKFKESREAAALNLAY 235

RESULT 18

US-09-906-838-137
; Sequence 137, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-137
Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 RLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSESE 52
Db 25 RLLSASDLRLRGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSESE 84
QY 53 DEQKLIERFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
Db 85 DEQKLIERFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144
QY 113 CGSEVCMVYHQPSPAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 172
Db 145 CGSEVCMVYHQPSPAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 204
QY 173 LTTVPVLPETQEDAKTKFKESREAAALNLAY 203
Db 205 LTTVPVLPETQEDAKTKFKESREAAALNLAY 235

RESULT 19

US-09-907-613-137
; Sequence 137, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-613-137

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKEACRRDGGQLVSI 52
Db 25 RLLSASDLRLGGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKEACRRDGGQLVSI 84

QY 53 DEQKLEKFIENLLPSDGFWDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
Db 85 DEQKLEKFIENLLPSDGFWDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144

QY 113 CGSEVCVMYHQPSAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETE 172
Db 145 CGSEVCVMYHQPSAPAGIGGYPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETE 204

QY 173 LTPVLPEETQEEDAKKTFKESREAAALNLAY 203
Db 205 LTPVLPEETQEEDAKKTFKESREAAALNLAY 235

RESULT 20
US-09-907-942-137
; Sequence 137, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-942-137

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKEACRRDGGQLVSI 52
Db 25 RLLSASDLRLGGQPVCRGGTQPCYKVIYFHDTSRRLNFEFEAKEACRRDGGQLVSI 84

QY 53 DEQKLEKFIENLLPSDGFWDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
Db 85 DEQKLEKFIENLLPSDGFWDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144

QY 113 CGSEVCVVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 172
Db 145 CGSEVCVVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 204
QY 173 LTTPLPEETQEDAKKTFKESREAAALNLAY 203
Db 205 LTTPLPEETQEDAKKTFKESREAAALNLAY 235

RESULT 21

US-09-904-859-137
; Sequence 137, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-859-137
Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSEIE 52
Db 25 RLLSASDLDRGGQPCVCRGGTQPCYKVIYFHDTSRLNPFEEAKEACRRDGGQLVSEIE 84
QY 53 DEQKLEKPIENLLPSDGDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYDEPS 112
Db 85 DEQKLEKPIENLLPSDGDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYDEPS 144
QY 113 CGSEVCVVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 172
Db 145 CGSEVCVVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 204
QY 173 LTTPLPEETQEDAKKTFKESREAAALNLAY 203
Db 205 LTTPLPEETQEDAKKTFKESREAAALNLAY 235

RESULT 22

US-09-909-204-137
; Sequence 137, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,204
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-204-137

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
Db 25 RLLSASDLRLGGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 84

QY 53 DEQKLIKFTIENLLPSDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
Db 85 DEQKLIKFTIENLLPSDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144

QY 113 CGSEVCVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETE 172
Db 145 CGSEVCVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETE 204

QY 173 LTTPLPEETQEDDAKKTFKESREAAALNLAY 203
Db 205 LTTPLPEETQEDDAKKTFKESREAAALNLAY 235

RESULT 23
US-09-904-820-137
; Sequence 137, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,820
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-820-137

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
Db 25 RLLSASDLRLGGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 84

QY 53 DEQKLIKFTIENLLPSDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112

Db 85 DEQKLEKFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144
QY 113 CGSEVCVVMYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 172
Db 145 CGSEVCVVMYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 204
QY 173 LTTPVLPEETQEEDAKKTFKESREAAALNLAY 203
Db 205 LTTPVLPEETQEEDAKKTFKESREAAALNLAY 235

RESULT 24
US-09-904-786-137
; Sequence 137, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,786
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo Sapien

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIIESE 52
Db 25 RLLSASDLRLRGQGPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIIESE 84
QY 53 DEQKLEKFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
Db 85 DEQKLEKFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144
QY 113 CGSEVCVVMYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 172
Db 145 CGSEVCVVMYHQPAPAGIGGYPYFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 204
QY 173 LTTPVLPEETQEEDAKKTFKESREAAALNLAY 203

Db 205 LTTPVLPEETQEEDAKKTFKESREAAALNLAY 235
RESULT 25
US-09-906-646-137
; Sequence 137, Application US/09906646
; Publication No. US20030039971A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,646
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-646-137

Query Match 98.7%; Score 1086; DB 10; Length 382;
Best Local Similarity 96.2%; Pred. No. 3.8e-101;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
Db |||||
25 RLLSASDLDLRGGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 84

QY 53 DEQKLIKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112
Db |||||
85 DEQKLIKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144

QY 113 CGSEVCVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETE 172
Db |||||
145 CGSEVCVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEETE 204

QY 173 LTTPLPEETQEEEDAKKTFKESREAAALNLAY 203
Db |||||
205 LTTPLPEETQEEEDAKKTFKESREAAALNLAY 235

Search completed: September 9, 2004, 23:13:11
Job time : 91.2776 secs

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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:50:45 ; Search time 15.9607 Seconds
(without alignments)
656.618 Million cell updates/sec

Title: US-09-887-855-2_COPY_25_227
Perfect score: 1100
Sequence: 1 RLLSGQPVCRGGTQPCYKV.....EEDAKTKFKESREALNLAY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1090	99.1	374	4	US-09-489-847-166 Sequence 166, Appli
2	1086	98.7	382	4	US-09-907-794A-137 Sequence 137, Appl
3	1086	98.7	382	4	US-09-905-125A-137 Sequence 137, Appl
4	1086	98.7	382	4	US-09-902-775A-137 Sequence 137, Appl
5	939.5	85.4	260	4	US-09-638-203-3 Sequence 3, Appli
6	561.5	51.0	273	4	US-09-638-203-2 Sequence 2, Appli
7	225	20.5	81	4	US-09-489-847-325 Sequence 325, App
8	225	20.5	82	4	US-09-489-847-234 Sequence 234, App
9	225	20.5	115	4	US-09-489-847-324 Sequence 324, App
10	182	16.5	1456	4	US-09-976-594-168 Sequence 168, App
11	178.5	16.2	1455	3	US-08-840-062-5 Sequence 5, Appli
12	176.5	16.0	1479	3	US-08-840-062-4 Sequence 4, Appli
13	174	15.8	1257	1	US-08-340-428B-49 Sequence 49, Appl
14	174	15.8	2409	6	5180808-2 Patent No. 5180808
15	170.5	15.5	1479	3	US-08-840-062-2 Sequence 2, Appli
16	152	13.8	912	5	PCT-US95-03747-2 Sequence 2, Appli
17	151	13.7	197	4	US-09-602-877A-99 Sequence 99, Appl
18	149.5	13.6	455	4	US-09-866-028-50 Sequence 50, Appl
19	149	13.5	174	1	US-07-641-971B-1 Sequence 1, Appli
20	149	13.5	174	1	US-07-781-248A-1 Sequence 1, Appli
21	149	13.5	320	1	US-08-365-103B-10 Sequence 10, Appl
22	149	13.5	321	1	US-08-365-103B-8 Sequence 8, Appli
23	148.5	13.5	652	2	US-08-751-305-2 Sequence 2, Appli
24	144.5	13.1	404	4	US-09-517-605-2 Sequence 2, Appli
25	143.5	13.0	372	2	US-08-513-278-4 Sequence 4, Appli
26	143.5	13.0	372	6	5514582-4 Patent No. 5514582
27	142	12.9	1487	3	US-08-840-062-7 Sequence 7, Appli

28	141.5	12.9	125	3	US-08-722-126A-7 Sequence 7, Appli
29	141.5	12.9	125	5	PCT-US95-04258-7 Sequence 7, Appli
30	141.5	12.9	287	1	US-08-365-103B-4 Sequence 4, Appli
31	141.5	12.9	300	1	US-08-365-103B-6 Sequence 6, Appli
32	141.5	12.9	327	1	US-08-365-103B-2 Sequence 2, Appli
33	138.5	12.6	117	6	5514582-7 Patent No. 5514582
34	138.5	12.6	119	1	US-08-340-539A-12 Sequence 12, Appl
35	137.5	12.5	110	6	5514582-12 Patent No. 5514582
36	137.5	12.5	123	6	5514582-19 Patent No. 5514582
37	137.5	12.5	492	4	US-09-724-864-39 Sequence 39, Appl
38	135	12.3	238	3	US-09-111-470-8 Sequence 8, Appli
39	134.5	12.2	128	4	US-09-535-521-8 Sequence 8, Appli
40	134.5	12.2	139	4	US-09-535-521-11 Sequence 11, Appl
41	134.5	12.2	141	4	US-09-535-521-14 Sequence 14, Appl
42	134.5	12.2	187	4	US-09-535-521-17 Sequence 17, Appl
43	134.5	12.2	208	4	US-09-535-521-20 Sequence 20, Appl
44	134.5	12.2	292	4	US-09-535-521-2 Sequence 2, Appli
45	134.5	12.2	292	4	US-09-535-521-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-489-847-166
; Sequence 166, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-489-847-166

Query Match 99.1%; Score 1090; DB 4; Length 374;
Best Local Similarity 99.0%; Pred. No. 9.5e-106;
Matches 201; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSI	EDEQKLI	60
DB	25	RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSI	EDEQKLI	84
QY	61	FIENLLPSDGDGFWIGLRRREKQSNSTACQDLYAWTDGSI	SQFRN	120
DB	85	FIENLLPSDGDGFWIGLRRREKQSNSTXCCQDLYAWTDGSI	SQFRN	144

QY 121 MYHQSAPAGIGPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 180
Db 145 MYHQSAPAGIGPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLPE 204
QY 181 ETQEEADAKTFKESREAAINLAY 203
Db 205 ETQEEADAKTFKESREAAINLAY 227

RESULT 2

US-09-907-794A-137
; Sequence 137, Application US/09907794A

; Patent No. 6635468

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,794A

; CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-137

Query Match 98.7%; Score 1086; DB 4; Length 382;

Best Local Similarity 96.2%; Pred. No. 2.6e-105;

Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLIS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEAAKEACRRDGGQLVSIIE 52

Db 25 RLISASDLRLGGQPCVCRGGTQPCYKVIYFHDTSRRLNFEAAKEACRRDGGQLVSIIE 84

QY 53 DEQKLEKFIENLLPSDGDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 112

Db 85 DEQKLEKFIENLLPSDGDGFWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS 144

QY 113 CGSEVCVMYHQPSPAPAGIGGYPMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 172

Db 145 CGSEVCVMYHQPSPAPAGIGGYPMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETE 204

QY 173 LTPVLPEETQEEADAKTFKESREAAINLAY 203

Db 205 LTPVLPEETQEEADAKTFKESREAAINLAY 235

RESULT 3

US-09-905-125A-137

; Sequence 137, Application US/09905125A

; Patent No. 6664376

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/905,125A

; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-137

Query Match 98.7%; Score 1086; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 2.6e-105;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
| | | | |
Db 25 RLLSASDLRLGCGQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 84
| | | | |
QY 53 DEQKLIKFIENLLPSDGFWDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRN 112
| | | | |
Db 85 DEQKLIKFIENLLPSDGFWDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRN 144
| | | | |
QY 113 CGSEVCVMYHQPAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAE 172
| | | | |
Db 145 CGSEVCVMYHQPAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAE 204
| | | | |
QY 173 LTPVLPEETQEEDAKTKTFKESREAAALNLAY 203
| | | | |
Db 205 LTPVLPEETQEEDAKTKTFKESREAAALNLAY 235
| | | | |

RESULT 4
US-09-902-775A-137
; Sequence 137, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-137

Query Match 98.7%; Score 1086; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 2.6e-105;
Matches 203; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 RLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 52
| | | | |
Db 25 RLLSASDLRLGCGQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI 84
| | | | |
QY 53 DEQKLIKFIENLLPSDGFWDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRN 112
| | | | |
Db 85 DEQKLIKFIENLLPSDGFWDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRN 144
| | | | |
QY 113 CGSEVCVMYHQPAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAE 172
| | | | |


```

; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (82)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-234

```

```
Query Match      20.5%; Score 225; DB 4; Length 82;
Best Local Similarity 100.0%; Pred.No. 3.6e-16;
Matches 41; Conservative 0; Mismatches 0; Indels
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Qy 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRR 41
25 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRR 65

Db

RESULT 9
 US-09-489-847-324
 ; Sequence 324, Application US/09489847
 ; Patent No. 6476195
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al
 ; TITLE OF INVENTION: 98 Human Secreted Proteins
 ; FILE REFERENCE: PZ031P1
 ; CURRENT APPLICATION NUMBER: US/09/489,847
 ; CURRENT FILING DATE: 2000-01-24
 ; EARLIER APPLICATION NUMBER: PCT/US99/17130
 ; EARLIER FILING DATE: 1999-07-29
 ; EARLIER APPLICATION NUMBER: 60/094,657
 ; EARLIER FILING DATE: 1998-07-30
 ; EARLIER APPLICATION NUMBER: 60/095,486
 ; EARLIER FILING DATE: 1998-08-05
 ; EARLIER APPLICATION NUMBER: 60/096,319
 ; EARLIER FILING DATE: 1998-08-12
 ; EARLIER APPLICATION NUMBER: 60/095,454
 ; EARLIER FILING DATE: 1998-08-06
 ; EARLIER APPLICATION NUMBER: 60/095,455
 ; EARLIER FILING DATE: 1998-08-06
 ; NUMBER OF SEQ ID NOS: 376
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 324
 ; LENGTH: 115
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-489-847-324

Query Match 20.5%; Score 225; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. NO. 5.7e-16;
Matches 41; Conservative 0; Mismatches 0; Indels

Qy 1 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRR 41
59 RLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRR 99

RESULT 10
US-09-976-594-168
; Sequence 168, Application US/09976594
; Patent No. 6673549

```

; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 168
; LENGTH: 1456
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1674368CD1
US-09-976-594-168

```

	Query Match	16.5%;	Score 182;	DB 4;	Length 1456;
	Best Local Similarity	25.5%;	Pred. No. 5.6e-10;		
	Matches 52; Conservative	37;	Mismatches 61;	Indels 54;	Gaps 8;
QY	18 YKVIYFHTSRRLNFEAAKEACRRDGGQLVSIESEDEQKLIEKFLENLLPSDGFWIGLR	77			
Dd	807 YKDYQYYFSKEKETMDNARAFCKRNFGLVSIQSESEKKFLWKYV-NRNDAQSAYFIGLL	865			
QY	78 RREEKQSNSTACQDLYAWTDGSGISQFRNWYVDPEPCGS--EVCVMYHQPSAPAGIGPY	135			
Dd	866 ISLDKK-----FAWMDGSKVDYVSWATGEPNFANEDENCVTMY----SNSGF----	908			
QY	136 MFQWNDRCNMKNFNICKYSDEK---PAVPSREAEGEETELTTPVLPEETQE-----	184			
Dd	909 ---WNDINGYPNAFICQRHNSINATTVPD-----TMPSPVPGCKEKGWNFYSN	954			
QY	185 -----EDAKKTFFKESREAL	199			
Dd	955 KCFXIFGMEFEERKNWOEARKACI	978			

RESULT 11
US-08-840-062-5
; Sequence 5, Application US/08840062
; Patent No. 6117977
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: WU, KAI
; TITLE OF INVENTION: TYPE C LECTINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,062
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1019R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881

TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-840-062-5

Query Match 16.2%; Score 178.5; DB 3; Length 1455;
Best Local Similarity 25.9%; Pred. No. 1.3e-09;
Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;

QY 18 YKVIYFHDTSRRRLNFEFEAKEACRRDGGQLVSI ESEDEQKLEKFIENLLPSDGFWIGLR 77
Db 806 YKDYQYYSKEKETMDNARRCKKNFGDLATIKSESEKFLWKYI-NKGGQSPYFIGWL 864
QY 78 RREEKQNSTACQDLYAWTDGSIQFRNMYVDEPSCGS--EVCVVMYHQSPAPAGIGGPY 135
Db 865 ISMDKK-----FIWMDGSKVDFVAVATGEPNFANDDENCVTMY-----TNSGF----- 907
QY 136 MFQWDDRCNMKNMFICK---YSDEKPAVPSREAGEETEITTPVLPEETQE----- 184
Db 908 ---WINDINGYPNNFICQHNSSINATAMP-----TTPTPGCKEGWHLYKNK 953
QY 185 -----EDAKTTFKESREAAALNL 201
Db 954 CFKIFGFANEKSKSWQDARQACKGL 978

RESULT 12
US-08-840-062-4
; Sequence 4, Application US/08840062
; Patent No. 611797
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: WU, KAI
; TITLE OF INVENTION: TYPE C LECTINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,062
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1019R1
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1479 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-840-062-4

Query Match 16.0%; Score 176.5; DB 3; Length 1479;
Best Local Similarity 30.4%; Pred. No. 2.2e-09;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;

QY 4 SGQVCRGGTQPCYKVIYFHDTSRRRLNFEFEAKEACRRDGGQLVSI ESEDEQKLEKFI E 63
Db 385 SWQPF-----QGH CYRL-----QA EKR SWQESKKACLRGGDLVSIHSM AELEFITKQIK 434
QY 64 NLLPSDGFWIGLR RREEKQNSTACQDLYAWTDGSIQFRNMYVDEPS---CGSEVCVV 120
Db 435 QEVE---ELWIGL-----NDLKLQMNFEWS DGLVSFTHWHPFEPNFRDSLEDCVT 483
QY 121 MYHQSPAPAGIGGPYMFQWDDRCNMKNMFICKYSDEKPAVPSREAE G 168
Db 484 IW----GPEG-----RWNDSPCNQSLPSICKKAGQLSQGAAAEEDHG 520

RESULT 13
US-08-340-428B-49
; Sequence 49, Application US/08340428B
; Patent No. 5648465
; GENERAL INFORMATION:
; APPLICANT: MARGOLIS, Richard U.
; APPLICANT: RAUCH, Uwe
; APPLICANT: MARGOLIS, Renee K.
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
; TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,428B
; FILING DATE: 14 No. 5648465ember 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/922,911
; FILING DATE: 03 August 1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: Margolis=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-340-428B-49

Query Match 15.8%; Score 174; DB 1; Length 1257;
Best Local Similarity 30.8%; Pred. No. 3.2e-09;
Matches 44; Conservative 18; Mismatches 49; Indels 32; Gaps 6;

QY 14 QRPCYKVIYFHDTSRRRLNFEFEAKEACRRDGGQLVSI ESEDEQKLEKFIENLLPSDGFW 73
Db 1037 QGH CYR--YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW 1085
QY 74 IGLRREEKQNSTACQDLYAWTDGSIQFRNMYVDEPS---CGSEVCVVMYHQSPAPAG 130
Db 1086 IGLNDRITVERD-----FQWTDNTGLQYENWREKQPDNFFAGGEDCVVMVAHENG--- 1134
QY 131 IGGPYMFQWDDRCNMKNMFICK 153

Db 1135 -----RWNDVPCNYNLPYCK 1150 :||| ||| :|||

RESULT 14

5180808-2

Patent No. 5180808

APPLICANT: RUOSLAHTI, ERKKI I.

TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID

SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN

ANTIBODIES, AND METHODS OF DETECTING THE SAME

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/441,179

FILING DATE: 27-NOV-1989

SEQ ID NO:2:

LENGTH: 2409

5180808-2

Query Match 15.8%; Score 174; DB 6; Length 2409;

Best Local Similarity 28.5%; Pred. No. 7.5e-09;

Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;

QY 14 QRPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSIIESEDEQKLIKFIENLLPSDGDGF- 72

Db 2190 QQCYK--YF---AHRRTWDAARECRLLQGAHLTSLSHEEQMFVNRV-----GHDYQ 2237

QY --73 WGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP---SCGSEVCVVMYHQPSAP 128

Db 2238 WIGL-----NDKMFEDHDFRWTGDTLQYENWRPNQDPSFFSAGEDCVVLIWHENG-- 2287

QY 129 AGIGGPFYMFQWDDRCNMKNFICKYS-----DEKPAVPSREAEGE 169

Db 2288 -----QWNDVPCNYHLTYTCKGTACGQPPVVENAKTFGK 2323

RESULT 15

US-08-840-062-2

Sequence 2, Application US/08840062

Patent No. 6117977

GENERAL INFORMATION:

APPLICANT: LASKY, LAURENCE A.

APPLICANT: WU, KAI

TITLE OF INVENTION: TYPE C LECTINS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/840,062

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P1019R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-3216

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1479 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-840-062-2

Query Match 15.5%; Score 170.5; DB 3; Length 1479;

Best Local Similarity 31.4%; Pred. No. 9.2e-09;

Matches 48; Conservative 22; Mismatches 48; Indels 35; Gaps 7;

QY 4 SQQPVCRGGTQRPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSIIESEDEQKLIKFI 63

Db 384 SQQPF-----QHCYRL-----QAEKRSWQESKRACLRGGDLLSIHSMAELEFITKQIK 433

QY 64 NLLPSDGDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS---CGSEVCVV 120

Db 434 QEVE---ELWIGL-----NDLKLQMFWSGSLVSFTTHWHPFEPNFRDLSLEDCVT 482

QY 121 MYHQPSAPAGIGGPFYMFQWDDRCNMKNFICK 153

Db 483 IW-----GPEG-----RWNDSPCNQSLPSICK 504

RESULT 16

PCT-US95-03747-2

Sequence 2, Application PC/TUS9503747

GENERAL INFORMATION:

APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION

TITLE OF INVENTION: Brevican, A Glial Cell Proteoglycan

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03747

FILING DATE: 27-MAR-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Imbra, Richard J.

REGISTRATION NUMBER: 37,643

REFERENCE/DOCKET NUMBER: PP-LJ 1453

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 912 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-03747-2

Query Match 13.8%; Score 152; DB 5; Length 912;

Best Local Similarity 28.8%; Pred. No. 4.1e-07;

Matches 47; Conservative 17; Mismatches 61; Indels 38; Gaps 8;

QY 14 QRPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSIIESEDEQKLIKFIENLLPSDGDGF 73

Db 697 QGACYK----HFSARR-SWEEAENKCRMYGAHLASISTPEEQDFINNRYREYQ-----W 745

QY 74 IGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS---CGSEVCVV- YHQPSAPA 129

Db 746 IGL-----NDRITGDFLWSDGVPLLYENWNPNQDPSYFLSGENCVVVMVHHDQG--- 794

QY 130 GIGGPFYMFQWDDRCNMKNFICKYS-----DEKPAVPSREAE 168

Db 795 -----QWSDVPCNYHLSTCKMGLVSCGPPPELPLAEVFG 829


```
RESULT 17
US-09-602-877A-99
; Sequence 99, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602.877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-602-877A-99

Query Match      13.7%; Score 151; DB 4; Length 197;
Best Local Similarity 25.0%; Pred. No. 6.5e-08;
Matches 38; Conservative 26; Mismatches 64; Indels 24; Gaps 4;

QY      6 QPVCRGGTQ--RPGYKVIYFHDTSRRLNFEAEKACRRDGGQGLVSISEDEQKLEKPIE 63
Db      65 QTVCLRGTKVHKCYLA-----SEGLKHFHEANEDCISKGGILVPRNSDEINALQDYCK 119

QY      64 NLLPSDGDFTWGLRRREKQSNSTACQDLYAWTDGSIQFRNMYVDEPSCGSEVCVVMYH 123
Db      120 RSLPGVNDFWLGI-----NDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFS 171

QY      124 QPSAPAGIGPGYMFQWNDRCNMKNNFICKYS 155
Db      172 QSA-----QGWKSDAEACRSKRYICEFT 194

RESULT 18
US-09-866-028-50
; Sequence 50, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866.028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 50
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-50
```

```
Query Match      13.6%; Score 149.5; DB 4; Length 455;
Best Local Similarity 25.6%; Pred. No. 2.9e-07;
Matches 45; Conservative 25; Mismatches 61; Indels 45; Gaps 8;

QY      11 GGTQPCYKVIY--FHDTSRRLN-----FEEAKEACRRDGGQGLVSISEDEQK 56
Db      287 GGAQ--CATKVHFPFHTCDLRIDGCFMVSEADTYRARMKQCRKGGVLAQIKSQKVQD 344

QY      57 LIEKFIENLLP-----SDGD-----FWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNMY 107
Db      345 ILAFYGLRLETTNEVTDSDFETRNFWIGLTYKTAK-----DSFRWATGEHQAFISPA 396

QY      108 VDEPSCGSEVCVVMYHQPSAPAGI-----GPYMFQWNDRCNMKNNFICKYSDE 157
Db      397 FGQPDNHGLVWL-----SAAMGFGNCVELQASAAFNWMDQCKTRNRYICQFAQE 446

RESULT 19
US-07-641-971B-1
; Sequence 1, Application US/07641971B
; Patent No. 5236706
; GENERAL INFORMATION:
; APPLICANT: Debre, Patrice
; APPLICANT: Mossalayi, Mohammed D
; TITLE OF INVENTION: A PHARMACEUTICAL PREPARATION FOR THE
; TITLE OF INVENTION: MATURATION OF PROTHYMOCYTES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation
; STREET: 556 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/641,971B
; FILING DATE: 19910116
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 90016254
; FILING DATE: 24-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fishman, Irving M
; REGISTRATION NUMBER: 30258
; REFERENCE/DOCKET NUMBER: 4-17921/+/DEB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-277-4832
; TELEFAX: 908-277-4306
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; CELL TYPE: Human B. Cells
; CELL LINE: CHO cells transformed with pCAL8-BF-ND
US-07-641-971B-1

Query Match      13.5%; Score 149; DB 1; Length 174;
Best Local Similarity 30.2%; Pred. No. 8.9e-08;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

QY      14 QRPCYKVIYFHDTSRRLNFEAEKACRRDGGQGLVSISEDEQKLEKFIENLLPSDGD 73
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Db 24 QKCY---YFGKGTQ--WVHARYACDDMEGQLVSIHSPPEQDFTLTKH-----ASHTGSW 73

QY 74 IGLRREEKQSNSTACQDLYAWTDGSGISQFRNWYVDEPSCGS--EVCVMYHQPSAPAGI 131

Db 74 IGLRNLDLKGE-----FIWVDGSHVDYSNWAPEPTSRSQGEDCVM-----RGS 118

QY 132 GGPYMFQWDDRCNMK--NNFICKYSDEKPAV---PSREAEGE-----ELETTPV 177

Db 119 G-----RWNDAFCDRKLGAWVC-----DRLATCTPPASEGSAESMGPDSPDPDGRLLTPS 169

QY 178 LP 179

Db 170 AP 171

RESULT 20

US-07-781-248A-1

; Sequence 1, Application US/07781248A

; Patent No. 5246699

; GENERAL INFORMATION:

; APPLICANT: Debre, Patrice

; APPLICANT: Mossalayi, Mohammed D

; TITLE OF INVENTION: MATURATION OF HEMATOPOIETIC CELLS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation

; STREET: 556 Morris Avenue

; CITY: Summit

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07901

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/781,248A

; FILING DATE: 19911230

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 90103565

; FILING DATE: 09-MAY-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Ikeler, Barbara J.

; REGISTRATION NUMBER: 36,170

; REFERENCE/DOCKET NUMBER: 4-18065/A/DEB

; TELEPHONE: 908-277-3368

; TELEFAX: 908-277-4306

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 174 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; CELL TYPE: Human B. Cells

; CELL LINE: CHO cells transformed with pCAL8-BF-ND

US-07-781-248A-1

Query Match 13.5%; Score 149; DB 1; Length 174;

Best Local Similarity 30.2%; Pred. No. 8.9e-08;

Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

QY 14 QRPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIHSEDEQKLIKFIENLLPSDGDWF 73

Db 24 QKCY---YFGKGTQ--WVHARYACDDMEGQLVSIHSPPEQDFTLTKH-----ASHTGSW 73

QY 74 IGLRREEKQSNSTACQDLYAWTDGSGISQFRNWYVDEPSCGS--EVCVMYHQPSAPAGI 131

Db 74 IGLRNLDLKGE-----FIWVDGSHVDYSNWAPEPTSRSQGEDCVM-----RGS 118

QY 132 GGPYMFQWDDRCNMK--NNFICKYSDEKPAV---PSREAEGE-----ELETTPV 177

Db 119 G-----RWNDAFCDRKLGAWVC-----DRLATCTPPASEGSAESMGPDSPDPDGRLLTPS 169

QY 178 LP 179

Db 170 AP 171

RESULT 21

US-08-365-103B-10

; Sequence 10, Application US/08365103B

; Patent No. 5766943

; GENERAL INFORMATION:

; APPLICANT: Lynch, Richard G

; APPLICANT: Nunez, Raphael D.

; APPLICANT: Yodoi, Jungi

; TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease

; STREET: 801 Grand Ave. Suite 3200

; CITY: Des Moines

; STATE: Iowa

; COUNTRY: United States

; ZIP: 50309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/365,103B

; FILING DATE: 28-DEC-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Nebel, Heidi S.

; REGISTRATION NUMBER: 37,719

; REFERENCE/DOCKET NUMBER: Uirf N5-24

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (515) 288-3667

; TELEFAX: (515) 288-1338

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 320 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-365-103B-10

Query Match 13.5%; Score 149; DB 1; Length 320;

Best Local Similarity 30.2%; Pred. No. 2e-07;

Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

QY 14 QRPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIHSEDEQKLIKFIENLLPSDGDWF 73

Db 170 QKCY---YFGKGTQ--WVHARYACDDMEGQLVSIHSPPEQDFTLTKH-----ASHTGSW 219

QY 74 IGLRREEKQSNSTACQDLYAWTDGSGISQFRNWYVDEPSCGS--EVCVMYHQPSAPAGI 131

Db 220 IGLRNLDLKGE-----FIWVDGSHVDYSNWAPEPTSRSQGEDCVM-----RGS 264

QY 132 GGPYMFQWDDRCNMK--NNFICKYSDEKPAV---PSREAEGE-----ELETTPV 177

Db 265 G-----RWNDAFCDRKLGAWVC-----DRLATCTPPASEGSAESMGPDSPDPDGRLLTPS 315

QY 178 LP 179

Query Match	13.0%;	Score 143.5;	DB 2;	Length 372;
Best Local Similarity	26.5%;	Pred. No. 9.4e-07;		
Matches 41;	Conservative 37;	Mismatches 50;	Indels 27;	Gaps 8;

Search completed: September 9, 2004, 22:58:16
Job time : 16.9607 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:39:44 ; Search time 85.7101 Seconds
(without alignments)
672.496 Million cell updates/sec

Title: US-09-887-855-2_COPY_24_227
Perfect score: 1106
Sequence: 1 GRLLSGQPVCRGSTRPCYK.....EEDAKTTFKESREALNLAY 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1106	100.0	374	3	AAY93948 Amino aci
2	1106	100.0	374	4	AAE03651 Human ext
3	1106	100.0	374	5	ABB90203 Human pol
4	1106	100.0	374	5	ABG66680 Human nov
5	1106	100.0	374	6	ADA54522 Human pro
6	1106	100.0	374	4	AAM25796 Human pro
7	1102	99.6	374	6	ADA54574 Human pro
8	1096	99.1	374	3	AAY91490 Human sec
9	1092	98.7	382	2	AAY13367 Amino aci
10	1092	98.7	382	3	ADC78457 Human PRO
11	1092	98.7	382	4	AAB80235 Human PRO
12	1092	98.7	382	4	AAU29033 Human PRO
13	1092	98.7	382	6	ABU58409 Human PRO
14	1092	98.7	382	6	ABU71613 Human PRO
15	1092	98.7	382	6	ABU87957 Novel hum
16	1092	98.7	382	6	ABU84272 Human sec
17	1092	98.7	382	6	ABR66146 Human sec
18	1092	98.7	382	6	ABR65536 Human sec
19	1092	98.7	382	6	ABU99476 Human sec
20	1092	98.7	382	6	ABU82715 Human PRO
21	1092	98.7	382	6	ABU89836 Novel hum
22	1092	98.7	382	6	ABU71468 Human PRO
23	1092	98.7	382	6	ABR68085 Human sec
24	1092	98.7	382	6	ABU96138 Novel hum
25	1092	98.7	382	6	ABU92569 Human sec

26	1092	98.7	382	6	ABO08646 Human sec
27	1092	98.7	382	6	ABO02698 Human sec
28	1092	98.7	382	6	ABR74852 Human sec
29	1092	98.7	382	6	ABR94614 Human sec
30	1092	98.7	382	6	ABU85587 Human PRO
31	1092	98.7	382	6	ABU98747 Novel hum
32	1092	98.7	382	6	ABU97962 Novel hum
33	1092	98.7	382	6	ABU91668 Novel hum
34	1092	98.7	382	6	ABU71914 Human sec
35	1092	98.7	382	6	ABU89361 Human PRO
36	1092	98.7	382	6	ABU86202 Human sec
37	1092	98.7	382	6	ABU67415 Human sec
38	1092	98.7	382	6	ABU80443 Human PRO
39	1092	98.7	382	6	ABO01797 Novel hum
40	1092	98.7	382	6	ABR99361 Human sec
41	1092	98.7	382	6	ABR98751 Human sec
42	1092	98.7	382	6	ABO16274 Human sec
43	1092	98.7	382	6	ABR92174 Human sec
44	1092	98.7	382	6	ABO18815 Human sec
45	1092	98.7	382	6	ABR78236 Human sec

ALIGNMENTS

RESULT 1
AAY93948
ID AAY93948 standard; protein; 374 AA.
XX AC AAY93948;
XX
DT 03-OCT-2000 (first entry)
XX
DE Amino acid sequence of a lectin ss3939 polypeptide.
XX
KW Human; lectin ss3939; chromosome 11; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21 /note= "signal peptide"
FT Domain 22..227 /note= "extracellular coding region"
FT Domain 228..248 /note= "predicted transmembrane domain"
FT Domain 249..374 /note= "predicted cytoplasmic or intracellular domain"

WO200039296-A1.

06-JUL-2000.

22-DEC-1999; 99WO-US030523.

23-DEC-1998; 98US-0113820P.

(IMMV) IMMUNEX CORP.

Anderson DA;

WPI; 2000-452394/39.

N-PSDB; AAA57382.

ss3939 nucleic acids, polypeptides and antibodies, useful for identifying human chromosome 11 and diseases associated with it.

Claim 12; Page 8; 73pp; English.

The present sequence represents a human lectin ss3939 polypeptide. The polynucleotide sequence is a source of probes, which may be used to identify nucleic acids encoding ss3939 proteins, to identify human chromosome number 11, to map genes on human chromosome number 11, to

CC identify diseases associated with chromosome 11, as single-stranded sense
CC or antisense oligonucleotides to inhibit expression of polypeptides
CC encoded by the ss3939 gene, and for gene therapy. The ss3939 polypeptides
CC may be useful for developing treatments for diseases (none specified)
CC associated with defective or insufficient amounts of the polypeptides.
CC The antibodies may be useful for detecting the presence of ss3939
CC polypeptides
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 1106; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e-104;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI ESEDEQKLI E 60
Db 24 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI ESEDEQKLI E 83
QY 61 KFIENLLPSDGDWFGLRRRREEKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGSEVCV 120
Db 84 KFIENLLPSDGDWFGLRRRREEKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGSEVCV 143
QY 121 VMYHQPAPAGIGGPGYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 180
Db 144 VMYHQPAPAGIGGPGYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 203
QY 181 EETQEDAKKTFKESREAAALNLAY 204
Db 204 EETQEDAKKTFKESREAAALNLAY 227

RESULT 2
AAE03651
ID AAE03651 standard; protein; 374 AA.
AC AAE03651;
XX 06-AUG-2001 (first entry)
XX Human extracellular matrix and cell adhesion molecule-15 (XMA-15).
XX Human; extracellular matrix and cell adhesion molecule; XMA-15;
KW gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia;
KW Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy;
KW sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma;
KW inflammatory disorder; acquired immune deficiency syndrome; AIDS;
KW Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma;
KW Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer;
KW glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis;
KW osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis;
KW infection; cell proliferative disorder; actinic keratosis; myeloma;
KW arteriosclerosis; nootropic; anticonvulsant; antithyroid; nephrotropic;
KW neuroprotective; dermatological.

XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1. .24 /label= Signal_peptide
FT Protein 25. .374 /note= "Mature human extracellular matrix and cell
FT adhesion molecule (XMA-15)"
FT Domain 46. .63 /note= "C-type lectin domain"
FT Domain 163. .176 /note= "C-type lectin domain"
FT Domain 224. .247 /note= "Transmembrane motif"
FT Domain 328. .348 /note= "Transmembrane motif"
XX WO200142285-A2.

PD 14-JUN-2001.
XX 05-DEC-2000; 2000WO-US032990.
XX 10-DEC-1999; 99US-0172852P.
PR 16-DEC-1999; 99US-0172354P.
XX (INCY-) INCYTE GENOMICS INC.
XX Yue H, Tang YT, Lal P, Burford N, Azimzai Y, Patterson C;
PI Baughn MR, Lu DAM, Shah P, Au-Young J;
XX WPI; 2001-381632/40.
DR N-PSDB; AAD08059.

XX New human extracellular matrix and cell adhesion molecules and
PT polynucleotide sequences encoding them, useful for diagnosis, prevention,
PT treatment of genetic, autoimmune and cell proliferative disorders.
XX Claim 1; Page 108-109; 135pp; English.

XX The present sequence is a human extracellular matrix and cell adhesion
CC molecule (XMA-15). The XMA-15 is used for screening a compound for
CC effectiveness as an agonist or antagonist of XMA-15. The identified agonist
CC or antagonist are used for treating a disease or condition associated
CC with decreased or increased expression of functional XMA-15. The
CC polynucleotides encoding XMA-15 are useful in somatic or germline gene
CC therapy to correct a genetic deficiency, to express a conditionally
CC lethal gene product and to express a protein which affords protection
CC against intracellular parasites and also for diagnosis of disorders
CC associated with expression of XMA-15. They are also used for generating
CC hybridisation probes useful in mapping the naturally occurring genomic
CC sequences and to create knock in humanised animals (pigs) or transgenic
CC animals (mice or rats) to model human diseases. Oligonucleotide or longer
CC fragments derived from the polynucleotide sequences may be used as
CC elements on a microarray. Antibodies which specifically bind XMA-15 may be
CC used for the diagnosis of disorders associated with the expression of
CC XMA-15, or in assays to monitor patients being treated with XMA-15. Diseases
CC diagnosed, prevented or treated include genetic disorders such as
CC adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's
CC disease, myotonic dystrophy, sickle cell anaemia, thalassaemia,
CC autoimmune/inflammatory disorders such as acquired immune deficiency
CC syndrome (AIDS), Addison's disease, allergies, anaemia, asthma,
CC atherosclerosis, Crohn's disease, diabetes mellitus, atopic dermatitis,
CC glomerulonephritis, multiple sclerosis, Grave's disease, osteoarthritis,
CC osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis,
CC bacterial, fungal, parasitic, protozoal and helminthic infections and
CC cell proliferative disorders such as actinic keratosis, arteriosclerosis
CC and cancer including breast, bladder, bone marrow, brain and uterus
CC cancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myeloma
XX Sequence 374 AA;

Query Match 100.0%; Score 1106; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e-104;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI ESEDEQKLI E 60
Db 24 GRLLSGQPVCRGGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI ESEDEQKLI E 83
QY 61 KFIENLLPSDGDWFGLRRRREEKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGSEVCV 120
Db 84 KFIENLLPSDGDWFGLRRRREEKQSNSTACQDLYAWTDGSI SQFRNWWYVDEPSCGSEVCV 143
QY 121 VMYHQPAPAGIGGPGYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 180
Db 144 VMYHQPAPAGIGGPGYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 203
QY 181 EETQEDAKKTFKESREAAALNLAY 204
Db 204 EETQEDAKKTFKESREAAALNLAY 227

RESULT 3
ABB90203
ID ABB90203 standard; protein; 374 AA.
XX
AC
XX
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2579.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnarary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
FN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US016450.
XX
PR 19-MAY-2000; 2000US-0205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
DR N-PSDB; ABL90612.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural; immune system, muscular, reproductive, and
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.
XX
PS Claim 11; SEQ ID NO 2579; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 374 AA;

Query Match
Best Local Similarity 100.0%; Score 1106; DB 5; Length 374;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRLLSGQPVCRGSTRPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSISEDEQKLI 60
DB 24 GRLLSGQPVCRGSTRPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSISEDEQKLI 83
QY 61 KFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
DB 84 KFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 143

QY 121 VMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTPVLP 180
DB 144 VMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAGEETELTPVLP 203
QY 181 EETQEDAKKTFKESREAAALNLAY 204
DB 204 EETQEDAKKTFKESREAAALNLAY 227

RESULT 4
ABG66680
ID ABG66680 standard; protein; 374 AA.
XX
AC ABG66680;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human novel polypeptide #15.
XX
KW Human; inflammatory condition; shock; sepsis; immune response; cancer;
KW wound healing; central nervous system disease; haematopoiesis;
KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
KW bone degenerative disorder; periodontal disease; reperfusion injury;
KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
KW allergic condition; thrombolysis; thrombosis; coagulation disorder;
KW fungal infection.
XX
OS Homo sapiens.
XX
PN WO200244340-A2.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US047004.
XX
PR 30-NOV-2000; 2000US-00728952.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;
PI Yamazaki V, Ujwal ML, Drmanac RT;
XX
DR WPI; 2002-508509/54.
DR N-PSDB; ABK94904.
XX
XX Novel nucleic acids and polypeptides for diagnosis, treatment of
PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
PT disorders, cancer and promoting wound healing.
XX
PS Claim 10; Page 579-580; 672pp; English.
XX
CC The invention relates to human novel polynucleotides and associated
CC polypeptides. The polynucleotides and polypeptides are useful for
CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
CC and cancer and for promoting wound healing. The sequences are used to
CC induce the proliferation of neural cells and regeneration of nerve and
CC brain tissue, and are useful for the treatment of central and peripheral
CC nervous system diseases and neuropathies, such as Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and amyotrophic lateral
CC sclerosis. The sequences are involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
CC cell disorders and platelet disorders such as thrombocytopenia,
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
CC disease. The sequences of the invention are also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia

CC gravis, allergic conditions such as asthma, thrombolysis or thrombosis
CC and coagulation disorders. Sequences ABG6666-ABG66758 represent human
CC novel polypeptides of the invention
XX
SQ Sequence 374 AA;
Query Match 100.0%; Score 1106; DB 5; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e-104;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSI ESEDEQKLI E 60
Db 24 GRLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSI ESEDEQKLI E 83
QY 61 KFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSI QFRNWWYVDEPSCGSEVCV 120
Db 84 KFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSI QFRNWWYVDEPSCGSEVCV 143
QY 121 VMYHQPSAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 180
Db 144 VMYHQPSAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 203
QY 181 EETQEEADAKTKFKESREAAALNLAY 204
Db 204 EETQEEADAKTKFKESREAAALNLAY 227
RESULT 5
ADA54522
ID ADA54522 standard; protein; 374 AA.
XX
AC ADA54522;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human protein, SEQ ID 2090.
XX
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX
OS Homo sapiens.
XX
PN EP1293569-A2.
XX
PD 19-MAR-2003.
XX
PF 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
PR 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hic Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-395539/38.
DR N-PSDB; ADA52883.
XX
FT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 14; SEQ ID NO 2090; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.

XX
SQ Sequence 374 AA;
Query Match 100.0%; Score 1106; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e-104;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSI ESEDEQKLI E 60
Db 24 GRLLSGQPVCRGGTQPCYKVIYFHDTSRRLNFEAEKACRRDGGQLVSI ESEDEQKLI E 83
QY 61 KFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSI QFRNWWYVDEPSCGSEVCV 120
Db 84 KFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSI QFRNWWYVDEPSCGSEVCV 143
QY 121 VMYHQPSAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 180
Db 144 VMYHQPSAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGETELTTPVLP 203
QY 181 EETQEEADAKTKFKESREAAALNLAY 204
Db 204 EETQEEADAKTKFKESREAAALNLAY 227
RESULT 6
AAM25796
ID AAM25796 standard; protein; 387 AA.
XX
AC AAM25796;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:1311.
XX
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiaggregant; haemostatic; vulnery; antiulcer; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antitense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder.
XX
OS Homo sapiens.
XX
PN WO200153455-A2.
XX
PD 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US035017.
PF 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457603/49.
DR N-PSDB; AAH99737.
XX
PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
XX
PS Claim 20; Page 272; 1217pp; English.

AAH999166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; anidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders

XX	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX	WPI: 2003-395539/38.
DR	N-PSDB; ADA52935.
DR	
XX	New polynucleotides encoding full-length polypeptides, e.g. secretory
PT	and/or membrane proteins, useful for developing medicines for diseases in
PT	which the gene is involved, or as target molecules for gene therapy.
PT	
XX	Claim 14; SEQ ID NO 2142; 205pp; English.
PS	
XX	The present invention relates to novel human secretory or membrane
CC	proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC	ADA54071). The coding sequences are useful in the gene therapy of
CC	diseases caused by abnormalities of the proteins, e.g. cancer,
CC	inflammatory diseases, osteoporosis or neurological disease.
CC	
XX	Sequence 374 AA;
SQ	

PA (HUMA-) HUMAN GENOME SCI INC.
XX Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX WPI; 2000-195282/17.
DR N-PSDB; AAA26385.
XX
XX New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
XX Claim 11; Page 483-484; 634pp; English.
PS
XX The polynucleotide sequences given in AAA26346 to AAA26458 encode the
CC human secreted proteins given in AAY91451 to AAY91691. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic;
CC immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective;
CC antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;
CC antiasthma; antipsoriatic; and cardiant. The polynucleotides and their
CC corresponding secreted proteins are useful for preventing, treating or
CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
CC pathological conditions can be diagnosed by determining the amount of the
CC proteins in a sample or by determining the presence of mutations in the
CC polynucleotides. Specific uses are described for each of the
CC polynucleotides, based on which tissues they are most highly expressed
CC in, and include developing products for the diagnosis or treatment of
CC cancer, tumours, neurodegenerative disorders, developmental abnormalities
CC and foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, inflammation, allergies,
CC Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,
CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
CC reproductive disorders, gastrointestinal disorders, respiratory disorders
CC and metabolic disorders. The proteins or polynucleotides can also be used
CC as food additives or preservatives. The proteins are also useful for
CC identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 374 AA;

Query Match 99.1%; Score 1096; DB 3; Length 374;
Best Local Similarity 99.0%; Pred. No. 3.4e-103;
Matches 202; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GRLLSGQPVCRGQTQPCYKVIYFHDTSRRRLNFEEAKEACRDGGQLVSI ESEDEQKLI E 60
Db 24 GRLLSGQPVCRGQTQPCYKVIYFHDTSRRRLNFEEAKEACRDGGQLVSI ESEDEQKLI E 83

QY 61 KFIENLLPSDGFQWIGLRRREKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 120
Db 84 XFIENLLPSDGFQWIGLRRREKQSNSTXCQDLYAWTDGSIQFRNWWYVDEPSCGSEVCV 143

QY 121 VMYHQPSAPAGIGGPFYMFQWNDRCNMKNFICKYSDCKPAVPSREAEGEETELTTPVLP 180
Db 144 VMYHQPSAPAGIGGPFYMFQWNDRCNMKNFICKYSDCKPAVPSREAEGEETELTTPVLP 203

QY 181 EETQEDAKKTFKESREALNLAY 204
Db 204 EETQEDAKKTFKESREALNLAY 227

RESULT 9
AAY13367
ID AAY13367 standard; protein; 382 AA.
XX AAY13367;
AC
XX
DT 25-JUN-1999 (first entry)
XX
DE Amino acid sequence of protein PRO234.

XX
KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
KW wound healing; tissue repair.
XX
XX Homo sapiens.
OS
XX WO9914328-A2.
PN
XX 25-NAR-1999.
PD
XX 16-SEP-1998; 98WO-US019330.
PF
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
XX
XX (GETH) GENENTECH INC.
XX
XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
PI
XX WPI; 1999-229533/19.
DR

DR N-PSDB; AAX52238.
XX
PT New isolated human genes and polypeptides used in, e.g. treatment of
PT gastrointestinal ulceration.
XX
PS Claim 12; Fig 50; 320pp; English.
XX
CC AAY13344-403 represent secreted and transmembrane human proteins. The
CC cDNA sequences are obtained from cDNA libraries, prepared from fetal
CC lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
CC encoded polypeptides have specific uses based on their homology to known
CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated
CC with the preservation and maintenance of gastrointestinal mucosa and the
CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
CC microvillus atrophy), skin diseases associated with abnormal keratinocyte
CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous
CC cell carcinoma of the vulva and gliomas), potent effects on cell growth
CC and development, diseases related to growth or survival of nerve cells
CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or
CC cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal
CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
CC have therapeutic applications in wound healing and tissue repair; PRO317
CC can be used for treating problems of the kidney, uterus, endometrium,
CC blood vessels, or related tissue, e.g. in the heart of genital tract
XX
SQ Sequence 382 AA;

Query Match 98.7%; Score 1092; DB 2; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 52
Db 24 GRLLSASDLDLRGGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 83

QY 53 EDEQKLIKFIENLLPSDGDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112
Db 84 EDEQKLIKFIENLLPSDGDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143

QY 113 SCGSEVCVVMYHQPSAPAGIGGPFYMFQWNDRCNMKNNFICKYSDEKPAVPSREAEGET 172
Db 144 SCGSEVCVVMYHQPSAPAGIGGPFYMFQWNDRCNMKNNFICKYSDEKPAVPSREAEGET 203

QY 173 ELTTPVLPEETQEEADAKKTFKESREAAALNLAY 204
Db 204 ELTTPVLPEETQEEADAKKTFKESREAAALNLAY 235

RESULT 10
ADC78457
ID ADC78457 standard; protein; 382 AA.
XX
AC ADC78457;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human PRO234 protein.
XX
KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
KW neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;
KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;
KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
KW diabetes; stroke; gene therapy; transgenic; PRO; human.
XX

OS Homo sapiens.
XX
PN WO200015796-A2.
XX
PD 23-MAR-2000.
XX
PF 15-SEP-1999; 99WO-US021090.
XX
PR 16-SEP-1998; 98WO-US019330.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
PI Yuan J;
XX
DR WPI; 2000-271434/23.
DR N-PSDB; ADC78456.
XX
PT Novel nucleic acids encoding secreted and transmembrane polypeptides with
PT homology, e.g. to growth and cancer-associated antigens.
XX
PS Claim 12; SEQ ID NO 137; 355pp; English.
XX
CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.
CC The polypeptides and polynucleotides of the invention may be useful as
CC research tools and as therapeutics for treating enterocolitis, Zollinger-
CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
CC scarring and wound healing, nerve repair, thrombosis, bone and/or
CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
CC infertility, premature aging, AIDS, diabetes complications and stroke.
CC The molecules may also be utilised during gene therapy procedures and
CC transgenic animal production. The current sequence is that of the human
CC PRO protein of the invention.
XX
SQ Sequence 382 AA;

Query Match 98.7%; Score 1092; DB 3; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 52
Db 24 GRLLSASDLDLRGGQPVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 83

QY 53 EDEQKLIKFIENLLPSDGDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112
Db 84 EDEQKLIKFIENLLPSDGDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143

QY 113 SCGSEVCVVMYHQPSAPAGIGGPFYMFQWNDRCNMKNNFICKYSDEKPAVPSREAEGET 172
Db 144 SCGSEVCVVMYHQPSAPAGIGGPFYMFQWNDRCNMKNNFICKYSDEKPAVPSREAEGET 203

QY 173 ELTTPVLPEETQEEADAKKTFKESREAAALNLAY 204
Db 204 ELTTPVLPEETQEEADAKKTFKESREAAALNLAY 235

RESULT 11
AAB80235
ID AAB80235 standard; protein; 382 AA.
XX
AC AAB80235;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PRO234 protein.
XX
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian neurotropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW

KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX

OS Homo sapiens.

XX WO200104311-A1.
PN

XX 19-JAN-2001.
PD

XX 22-FEB-2000; 2000WO-US004414.
PF

XX 07-JUL-1999; 99US-0143048P.
PR

PR 26-JUL-1999; 99US-0145698P.
PR

PR 28-JUL-1999; 99US-0146222P.
PR

PR 08-SEP-1999; 99WO-US020594.
PR

PR 13-SEP-1999; 99WO-US020944.
PR

PR 15-SEP-1999; 99WO-US021090.
PR

PR 15-SEP-1999; 99WO-US021547.
PR

PR 05-OCT-1999; 99WO-US023089.
PR

PR 29-NOV-1999; 99WO-US028214.
PR

PR 30-NOV-1999; 99WO-US028313.
PR

PR 02-DEC-1999; 99WO-US028564.
PR

PR 02-DEC-1999; 99WO-US028565.
PR

PR 16-DEC-1999; 99WO-US030095.
PR

PR 20-DEC-1999; 99WO-US030911.
PR

PR 20-DEC-1999; 99WO-US030999.
PR

PR 05-JAN-2000; 2000WO-US000219.
PR

XX (GETH) GENENTECH INC.
PA

XX Ashkenazi AJ, Botstein D, Desnovers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;

XX WPI; 2001-081051/09.
DR

DR N-PSDB; AAF72396.
DR

XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).

XX Claim 1; Fig 50; 393pp; English.
PS

XX The present sequence is one of sixty one novel secreted and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful for treating skin
CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC infertility, AIDS and diabetes and retinal disorders such as retinitis
CC pigmentosum. The PRO nucleic acids have applications in molecular
CC biology, including use as hybridization probes, and in chromosome and
CC gene mapping

XX Sequence 382 AA;
SQ

Query Match 98.7%; Score 1092; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIES 52
DB |||||

DB 24 GRLLSASDLDRGGQPVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIES 83
|||

QY 53 EDEQKLIKFIENLLPSDGFWIGLRRREKQSNSTACQDLAWTSGISQFRNYYVDEP 112
DB |||||

DB 84 EDEQKLIKFIENLLPSDGFWIGLRRREKQSNSTACQDLAWTSGISQFRNYYVDEP 143
|||

QY 113 SCGSEVCVMYHQPAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEET 172
DB |||||

DB 144 SCGSEVCVMYHQPAPAGIGGPPYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEET 203
|||

QY 173 ELTTPVLPEETOEDAKKTFKESREAAALNLAY 204
DB |||||

DB 204 ELTTPVLPEETOEDAKKTFKESREAAALNLAY 235
|||

RESULT 12
AAU29033

ID AAU29033 standard; protein; 382 AA.
XX

AC AAU29033;
XX

DT 18-DEC-2001 (first entry)
XX

DE Human PRO polypeptide sequence #10.
XX

KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX

OS Homo sapiens.
XX

PN WO200168848-A2.
XX

PD 20-SEP-2001.
XX

PF 28-FEB-2001; 2001WO-US006520.
XX

PR 01-MAR-2000; 2000WO-US005601.
PR

PR 02-MAR-2000; 2000WO-US005841.
PR

PR 03-MAR-2000; 2000US-0187202P.
PR

PR 06-MAR-2000; 2000US-0186968P.
PR

PR 14-MAR-2000; 2000US-0189320P.
PR

PR 14-MAR-2000; 2000US-0189328P.
PR

PR 15-MAR-2000; 2000WO-US006884.
PR

PR 21-MAR-2000; 2000US-0190828P.
PR

PR 21-MAR-2000; 2000US-0191007P.
PR

PR 21-MAR-2000; 2000US-0191048P.
PR

PR 21-MAR-2000; 2000US-0191314P.
PR

PR 28-MAR-2000; 2000US-0192655P.
PR

PR 29-MAR-2000; 2000US-0193032P.
PR

PR 29-MAR-2000; 2000US-0193053P.
PR

PR 30-MAR-2000; 2000WO-US008439.
PR

PR 04-APR-2000; 2000US-0194449P.
PR

PR 04-APR-2000; 2000US-0194647P.
PR

PR 11-APR-2000; 2000US-0195975P.
PR

PR 11-APR-2000; 2000US-0196000P.
PR

PR 11-APR-2000; 2000US-0196187P.
PR

PR 11-APR-2000; 2000US-0196690P.
PR

PR 11-APR-2000; 2000US-0196820P.
PR

PR 18-APR-2000; 2000US-0198121P.
PR

PR 18-APR-2000; 2000US-0198585P.
PR

PR 25-APR-2000; 2000US-0199397P.
PR

PR 25-APR-2000; 2000US-0199550P.
PR

PR 25-APR-2000; 2000US-0199654P.
PR

PR 03-MAY-2000; 2000US-0201516P.
PR

PR 17-MAY-2000; 2000WO-US013705.
PR

PR 22-MAY-2000; 2000WO-US014042.
PR

PR 30-MAY-2000; 2000WO-US014941.
PR

PR 02-JUN-2000; 2000WO-US015264.
PR

PR 05-JUN-2000; 2000US-0209832P.
PR

PR 28-JUL-2000; 2000WO-US020710.
PR

PR 22-AUG-2000; 2000US-00644848.
PR

PR 24-AUG-2000; 2000WO-US023328.
PR

PR 08-NOV-2000; 2000WO-US030952.
PR

PR 01-DEC-2000; 2000WO-US032678.
PR

PR 20-DEC-2000; 2000WO-US034956.
XX

(GETH) GENENTECH INC. PA

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-602746/68.
DR N-PSDB; AAS45934.
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX Claim 11; Fig 20; 774pp; English.
PS Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
XX The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX Sequence 382 AA;
SQ Query Match 98.7%; Score 1092; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 GRLLS-----GQVCRGGTORPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSIES 52
Db |||||
24 GRLLSASDLRLRGQPVCRGGTORPCYKVIYFHDTSRRLNFEFEAKACRRDGGQLVSIES 83
QY 53 EDEQKLIKFIENLLPSDGFWIGLRRRREKQSNSTACODLYAWTDGSIQFRNWWYVDEP 112
Db |||||
84 EDEQKLIKFIENLLPSDGFWIGLRRRREKQSNSTACODLYAWTDGSIQFRNWWYVDEP 143
QY 113 SCGSEVCVMYHQPSAPAGIGGPFQWNDRCNMKNFICKYSDEKPAVPSREAEGEET 172
Db |||||
144 SCGSEVCVMYHQPSAPAGIGGPFQWNDRCNMKNFICKYSDEKPAVPSREAEGEET 203
QY 173 ELTTPVLPEETQEEDAKKTFKESREAAALNLAY 204
Db |||||
204 ELTTPVLPEETQEEDAKKTFKESREAAALNLAY 235
RESULT 13
ABU58409
ID ABU58409 standard; protein; 382 AA.
XX AC ABU58409;
XX DT 15-APR-2003 (first entry)
XX DE Human PRO polypeptide #10.
XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX PN US2003027272-A1.
XX PD 06-FEB-2003.
XX

PF 21-JUN-2002; 2002US-00176492.
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078866P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
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PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
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PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
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PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
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PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 98.7%; Score 1092; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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QY 53 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYDEP 112
Db |||||
84 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYDEP 143

QY 113 SCGSEVCVVMYHQPSAPAGIGGPFQWDDRCNMKNFNCKYSDEKPAVPSREAEGEET 172
Db |||||
144 SCGSEVCVVMYHQPSAPAGIGGPFQWDDRCNMKNFNCKYSDEKPAVPSREAEGEET 203

QY 173 ELTTPVLPEETQEEDAKKTFKESREAAALNLAY 204
Db |||||
204 ELTTPVLPEETQEEDAKKTFKESREAAALNLAY 235

RESULT 14
ABU71613

ID ABU71613 standard; protein; 382 AA.

XX ABU71613;
AC ABU71613;

XX
DT 16-JUN-2003 (first entry)
XX

DE Human PRO polypeptide #24.
XX

KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW pathological disorder; cardiac insufficiency disorder; protein secretion;
KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;

KW cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal;
XX antiulcer; dermatological; vulnery.

OS Homo sapiens.

XX US2002146709-A1.

PN 10-OCT-2002.

PD 18-JUL-2001; 2001US-00909088.

XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
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PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
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PR 31-OCT-1997; 97US-0063970P.
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PR 03-NOV-1997; 97US-0064248P.
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PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
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PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US02108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

XX (GETH) GENENTECH INC.

XX PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;

XX WPI; 2003-328338/31.
DR N-PSDB; ACA59008.

PT Isolated nucleic acid useful for e.g., treating pathological disorders
PT encodes a secreted or transmembrane protein.

XX Claim 12; Fig 50; 473pp; English.

XX The invention relates to human PRO polypeptides (secreted or
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC PRO polypeptides and polynucleotides can be used in treating pathological
CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
CC disorders and in therapeutic treatment of disorders involving protein
CC secretion by the pancreas, including diabetes. They can also be used in
CC treating disorders associated with the preservation and maintenance of
CC gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, and skin diseases associated with abnormal keratinocyte
CC differentiation (e.g., psoriasis, epithelial cancers such as lung
CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
CC The sequences can be used as molecular markers for protein
CC electrophoresis purposes and can be utilised in protein-protein binding
CC assays, biochemical screening assays, immuncassays and cell-based assays.
CC This sequence represents a human PRO polypeptide of the invention

XX SQ Sequence 382 AA;

Query Match 98.7%; Score 1092; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLIS-----GQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 52
Db 24 GRLISASDLDRGGQPVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 83
QY 53 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112
Db 84 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143
QY 113 SCGSEVCVMYHQPSAPAGICGPPYMFQWNDRCNMKNPFICKYSDEKPAVPSREAEGET 172
Db 144 SCGSEVCVMYHQPSAPAGICGPPYMFQWNDRCNMKNPFICKYSDEKPAVPSREAEGET 203
QY 173 ELTTPVLPEETOEDAKKTFKESREALNLAY 204
Db 204 ELTTPVLPEETOEDAKKTFKESREALNLAY 235

RESULT 15
ABU87957
ID ABU87957 standard; protein; 382 AA.
XX
AC ABU87957;
XX
DT 07-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO234.
XX
KW Human; secreted and transmembrane protein: PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
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PR	01-OCT-1998;	98US-0102684P;
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Qy	173	ELTTPVLPEETQBEDAKKTFKESREAA	204
Db	204	ELTTPVLPEETQBEDAKKTFKESREAA	235
RESULT 16			
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ID	ABU84272	standard; protein; 382 AA.	
XX			
AC	ABU84272;		
XX			
DT	02-AUG-2003	(first entry)	
XX			
DE	Human secreted/transmembrane protein (PRO)	#10.	
XX			
KW	Human; secreted and transmembrane protein; PRO;		
KW	tumour necrosis factor alpha; chondrocyte cell;		
KW	tissue typing.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003032112-A1.		
XX			
PD	13-FEB-2003.		
XX			
PF	21-JUN-2002; 2002US-00176756.		
XX			
PR	18-SEP-1997;	97US-0059263P.	
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PR 10-SEP-1998; 98US-0099741P.
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PR 30-SEP-1998; 98US-0102570P.
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PR 01-OCT-1998; 98US-0102684P.
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Query Match 98.7%; Score 1092; DB 6; Length 382;

Best Local Similarity 96.2%; Pred. No. 9e-103;

Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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Qy 53 EDEQKLI EKFIENLLPSDGFWIGLRRRREKQSNSTACQDLYAWTDGSIQFRNWIYVDEP 112

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PR 24-JUL-1998; 98US-0094006P.
PR 04-AUG-1998; 98US-0095282P.
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PR 17-AUG-1998; 98US-0096757P.
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PR 17-AUG-1998; 98US-0096897P.
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PR 02-SEP-1998; 98US-0098803P.
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PR 09-SEP-1998; 98US-0099602P.
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PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
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PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
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PR 01-OCT-1998; 98US-0102684P.
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Query Match 98.7%; Score 1092; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 GRLLS-----GQPVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIES 52
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Db 24 GRLLSASDLRLGGQPVCRGGTQPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIES 83
QY 53 EDEQKLIKFIENLLPSDGDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWIYVDEP 112
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QY 113 SCGSEVCVVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGEET 172
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QY 173 ELTTPVLPEETQEEDAKKTFKESREAAINLAY 204
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Db 204 ELTTPVLPEETQEEDAKKTFKESREAAINLAY 235
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RESULT 18

ABR65536
ID ABR65536 standard; protein; 382 AA.
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AC ABR65536;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO234, SEQ ID NO:20.
XX
KW Human; PRO; secreted protein; transmembrane protein;
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulnery; gene therapy.

OS Homo sapiens.
XX
PN US2003036159-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00188773.
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PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
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PR 28-OCT-1997; 97US-0063540P.
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PR 24-JUL-1998; 98US-0094006P.
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PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
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PR 18-AUG-1998; 98US-0096959P.
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PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
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PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
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PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
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PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match

98.7%; Score 1092; DB 6; Length 382;

Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 GRLLS-----GQVCRGGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSIES 52
Db 24 GRLLSASDLDLRGQPVCRGGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSIES 83
QY 53 EDEQKLEKFIENLLPSDGDFTWGLRRREEKQSNSTACODLYAWTDGSIQPRNWWYVDEP 112
Db 84 EDEQKLEKFIENLLPSDGDFTWGLRRREEKQSNSTACODLYAWTDGSIQPRNWWYVDEP 143
QY 113 SCGSEVCVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSPRAEAGEET 172
Db 144 SCGSEVCVMYHQPSAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSPRAEAGEET 203
QY 173 ELTTPVLPEETOEDAKKTFKESRRAALNLAY 204
Db 204 ELTTPVLPEETOEDAKKTFKESRRAALNLAY 235

RESULT 19
ABU99476
ID ABU99476 standard; protein; 382 AA.
XX AC ABU99476;
XX DT 09-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #10.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX OS Homo sapiens.
XX PN US2003040070-A1.
XX PD 27-FEB-2003.
XX PF 27-JUN-2002; 2002US-00184627.
XX PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
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PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
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XX
KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
chromosome mapping; gene mapping; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003032113-A1.
PD 13-FEB-2003.
XX
PF 20-JUN-2002; 2002US-00176911.
XX

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PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
PR WPI; 2003-361832/34.

DR N-PSDB; ACA58405.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 12; Fig 50; 474pp; English.
XX
CC The present invention relates to the isolation of novel human secreted
CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
CC sequences encoding them. The polynucleotide sequences are useful in
CC molecular biology, as hybridisation probes, in chromosome and gene
CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide sequences may also be used in preparing PRO polypeptides
CC by recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptides or
CC their antibodies are useful in preparing a medicament for treating a
CC condition responsive to the polypeptide or antibody, such as cancer,
CC Alzheimer's disease or ischaemia, and in various diagnostic assays.
CC ABU71445-ABU71505 represent human PRO polypeptides of the invention
XX
SQ Sequence 382 AA;

Query Match 98.7%; Score 1092; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSIES 52
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Db 24 GRLLSASDLDLRGGQPCVCRGGTQPCYKVIYFHDTSRRLNFEAEACRRDGGQLVSIES 83

QY 53 EDEQKLEKFIENLLPSDGFWIGLRRREEKQNSTACQDLYAWTDGSIQFRNMYVDEP 112
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Db 84 EDEQKLEKFIENLLPSDGFWIGLRRREEKQNSTACQDLYAWTDGSIQFRNMYVDEP 143

QY 113 SCGSEVCVMYHQPSAPAGIGGPFYMFQWDDRCNNKNNFICKYSDEKPAVPSRAEGEET 172
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Db 144 SCGSEVCVMYHQPSAPAGIGGPFYMFQWDDRCNNKNNFICKYSDEKPAVPSRAEGEET 203

QY 173 ELTPVLPEETQEDAKKTFKESREAAALNLAY 204
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Db 204 ELTPVLPEETQEDAKKTFKESREAAALNLAY 235

RESULT 23
ABR68085
ID ABR68085 standard; protein; 382 AA.
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AC ABR68085;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO234, SEQ ID NO:20.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027264-A1.
XX
PD 06-FEB-2003.
XX
PF 18-JUN-2002; 2002US-00174579.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.

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PR	21-OCT-1997;	97US-0063486P.	PR	10-JUN-1998;	98US-0088824P.
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PR	24-OCT-1997;	97US-0063121P.	PR	10-JUN-1998;	98US-0088826P.
PR	28-OCT-1997;	97US-0063540P.	PR	11-JUN-1998;	98US-0088861P.
PR	28-OCT-1997;	97US-0063541P.	PR	11-JUN-1998;	98US-0088863P.
PR	28-OCT-1997;	97US-0063544P.	PR	11-JUN-1998;	98US-0088876P.
PR	28-OCT-1997;	97US-0063564P.	PR	12-JUN-1998;	98US-0089090P.
PR	29-OCT-1997;	97US-0063734P.	PR	12-JUN-1998;	98US-0089105P.
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PR	08-APR-1998;	98US-0081070P.	PR	25-JUN-1998;	98US-0090696P.
PR	09-APR-1998;	98US-0081195P.	PR	26-JUN-1998;	98US-00105413.
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PR	21-APR-1998;	98US-0082568P.	PR	26-JUN-1998;	98US-0090863P.
PR	21-APR-1998;	98US-0082569P.	PR	26-JUN-1998;	98US-0090863P.
PR	22-APR-1998;	98US-0082704P.	PR	01-JUL-1998;	98US-0091010P.
PR	22-APR-1998;	98US-0082797P.	PR	01-JUL-1998;	98US-0091359P.
PR	28-APR-1998;	98US-0083322P.	PR	02-JUL-1998;	98US-0091544P.
PR	29-APR-1998;	98US-0083495P.	PR	02-JUL-1998;	98US-0091478P.
PR	29-APR-1998;	98US-0083496P.	PR	02-JUL-1998;	98US-0091486P.
PR	29-APR-1998;	98US-0083499P.	PR	02-JUL-1998;	98US-0091626P.
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PR	06-MAY-1998;	98US-0084414P.	PR	24-JUL-1998;	98US-0094006P.
PR	07-MAY-1998;	98US-0084639P.	PR	04-AUG-1998;	98US-0095282P.
PR	07-MAY-1998;	98US-0084640P.	PR	10-AUG-1998;	98US-0095998P.
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PR	18-MAY-1998;	98US-0086023P.	PR	17-AUG-1998;	98US-0096897P.
PR	22-MAY-1998;	98US-0086392P.	PR	18-AUG-1998;	98US-0096949P.
PR	22-MAY-1998;	98US-0086486P.	PR	18-AUG-1998;	98US-0096959P.
PR	28-MAY-1998;	98US-0087098P.	PR	18-AUG-1998;	98US-0097022P.
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PR	03-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097971P.
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PR	16-SEP-1998;	98WO-US019330.
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PR	30-SEP-1998;	98US-0102570P.
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<div>Query Match 98.7%; Score 1092; DB 6; Length 382; Best Local Similarity 96.2%; Pred. No. 9e-103; Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;</div>		
QY	1	GRLLS-----GQVCRGGTQPCYKVIYFHTSRRLNFEFEAKACRRDGGQLVSIES 52
Db	24	GRLLSASDLDLRGGQPVCRGGTQPCYKVIYFHTSRRLNFEFEAKACRRDGGQLVSIES 83
QY	53	EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112
Db	84	EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143
QY	113	SCGSEVCVMYHQPAPAGIGGPFMFQWDDRCNMKNFICKYSDEKPAVPSREAEGET 172
Db	144	SCGSEVCVMYHQPAPAGIGGPFMFQWDDRCNMKNFICKYSDEKPAVPSREAEGET 203
QY	173	ELTTPVLPEETOEDAKKTFKESREAAALNLAY 204
Db	204	ELTTPVLPEETOEDAKKTFKESREAAALNLAY 235
<div>RESULT 24 ABU96138 ID ABU96138 standard; protein; 382 AA. XX AC ABU96138; XX DT 25-JUL-2003 (first entry) XX DE Novel human secreted and transmembrane protein PRO234. XX KW Human; secreted and transmembrane protein; PRO; transgenic animal; KW knockout; chromosome identification; tissue typing; tumour; KW chondrocyte proliferation; chondrocyte differentiation; KW tumor necrosis factor-alpha release stimulator. XX OS Homo sapiens. XX PN US2003036144-A1. XX PD 20-FEB-2003. XX PF 01-JUL-2002; 2002US-00187601. XX</div>		

PR	18-SEP-1997;	97US-0059263P.
PR	18-SEP-1997;	97US-0059266P.
PR	17-OCT-1997;	97US-0062250P.
PR	21-OCT-1997;	97US-0063486P.
PR	24-OCT-1997;	97US-0063120P.
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Query Match 98.7%; Score 1092; DB 6; Length 382;
Best Local Similarity 96.2%; Pred. No. 9e-103;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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QY 53 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYDEP 112
Db |||||
84 EDEQKLIKFIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYDEP 143
QY 113 SCGSEVCVVMYHQPAPAGIGGYPYMFQWDDRCNMKNFNICKYSDKPAVPSREAEGET 172
Db |||||
144 SCGSEVCVVMYHQPAPAGIGGYPYMFQWDDRCNMKNFNICKYSDKPAVPSREAEGET 203
QY 173 ELTTPVLPEETOEDAKKTFKESREAAALNLAY 204
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RESULT 25
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XX
AC ABU92569;
XX
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DT 18-JUL-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) #10.
DE
XX Human; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cell; TNF-alpha;
KW tumour necrosis factor-alpha; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036149-A1.
XX

PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00187746.
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PR 18-SEP-1997; 97US-0059263P.
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PR	16-SEP-1998;	98WO-US019330.
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PR	25-SEP-1998;	98US-0101786P.
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PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-00168978.
Query Match 98.7%; Score 1092; DB 6; Length 382;		
Best Local Similarity 96.2%; Pred. No. 9e-103;		
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;		
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OM protein - protein search, using sw model

Run on: September 9, 2004, 22:50:45 ; Search time 16.0393 Seconds
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656.618 Million cell updates/sec

Title: US-09-887-855-2_COPY_24_227
Perfect score: 1106
Sequence: 1 GRLLSGQPVCRRGTQPCYK.....EEDAKKTFKESREALNLAY 204

Scoring table: BLOSUM62
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1096	99.1	374	4	US-09-489-847-166 Sequence 166, App
2	1092	98.7	382	4	US-09-907-794A-137 Sequence 137, App
3	1092	98.7	382	4	US-09-905-125A-137 Sequence 137, App
4	1092	98.7	382	4	US-09-902-775A-137 Sequence 137, App
5	939.5	84.9	260	4	US-09-638-203-3 Sequence 3, Appli
6	561.5	50.8	273	4	US-09-638-203-2 Sequence 2, Appli
7	231	20.9	81	4	US-09-489-847-325 Sequence 325, App
8	231	20.9	82	4	US-09-489-847-234 Sequence 234, App
9	231	20.9	115	4	US-09-489-847-324 Sequence 324, App
10	182	16.5	1456	4	US-09-976-594-168 Sequence 168, App
11	178.5	16.1	1455	3	US-08-840-062-5 Sequence 5, Appli
12	176.5	16.0	1479	3	US-08-840-062-4 Sequence 4, Appli
13	174	15.7	1257	1	US-08-340-428B-49 Sequence 49, Appl
14	174	15.7	2409	6	5180808-2 Patent No. 5180808
15	170.5	15.4	1479	3	US-08-840-062-2 Sequence 2, Appli
16	152	13.7	912	5	PCT-US95-03747-2 Sequence 2, Appli
17	151	13.7	197	4	US-09-602-877A-99 Sequence 99, Appl
18	149.5	13.5	455	4	US-09-866-028-50 Sequence 50, Appl
19	149	13.5	174	1	US-07-641-971B-1 Sequence 1, Appli
20	149	13.5	174	1	US-07-781-248A-1 Sequence 1, Appli
21	149	13.5	320	1	US-08-365-103B-10 Sequence 10, Appl
22	149	13.5	321	1	US-08-365-103B-8 Sequence 8, Appli
23	148.5	13.4	652	2	US-08-751-305-2 Sequence 2, Appli
24	144.5	13.1	404	4	US-09-517-605-2 Sequence 2, Appli
25	143.5	13.0	372	2	US-08-513-278-4 Sequence 4, Appli
26	143.5	13.0	372	6	5514582-4 Patent No. 5514582
27	142	12.8	1487	3	US-08-840-062-7 Sequence 7, Appli

28	141.5	12.8	125	3	US-08-722-126A-7 Sequence 7, Appli
29	141.5	12.8	125	5	PCT-US95-04258-7 Sequence 7, Appli
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31	141.5	12.8	300	1	US-08-365-103B-6 Sequence 6, Appli
32	141.5	12.8	327	1	US-08-365-103B-2 Sequence 2, Appli
33	138.5	12.5	117	6	5514582-7 Patent No. 5514582
34	138.5	12.5	119	1	US-08-340-539A-12 Sequence 12, Appl
35	137.5	12.4	110	6	5514582-12 Patent No. 5514582
36	137.5	12.4	123	6	5514582-19 Patent No. 5514582
37	137.5	12.4	492	4	US-09-724-864-39 Sequence 39, Appl
38	135	12.2	238	3	US-09-111-470-8 Sequence 8, Appli
39	134.5	12.2	128	4	US-09-535-521-11 Sequence 8, Appli
40	134.5	12.2	139	4	US-09-535-521-11 Sequence 11, Appl
41	134.5	12.2	141	4	US-09-535-521-14 Sequence 14, Appl
42	134.5	12.2	187	4	US-09-535-521-17 Sequence 17, Appl
43	134.5	12.2	208	4	US-09-535-521-20 Sequence 20, Appl
44	134.5	12.2	292	4	US-09-535-521-2 Sequence 2, Appli
45	134.5	12.2	292	4	US-09-535-521-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
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; Sequence 166, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-489-847-166

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Best Local Similarity 99.0%; Pred. No. 2e-106;
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RESULT 2

US-09-907-794A-137
; Sequence 137, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
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; PRIOR FILING DATE: 1999-10-05
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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911

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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
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; ORGANISM: Homo sapiens
US-09-907-794A-137

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Best Local Similarity 96.2%; Pred. No. 5.5e-106;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
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RESULT 3

US-09-905-125A-137
; Sequence 137, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-137

Query Match 98.7%; Score 1092; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 5.5e-106;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 52
Db 24 GRLLSASDLDLRGGQPCVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 83

QY 53 EDEQKLIKFIENLLPSDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112
Db 84 EDEQKLIKFIENLLPSDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143

QY 113 SCGSEVCVVMYHQPAPAGIGGPFYMFQWNDRCNMKNNFICKYSDEKPAVPSREAEGET 172
Db 144 SCGSEVCVVMYHQPAPAGIGGPFYMFQWNDRCNMKNNFICKYSDEKPAVPSREAEGET 203

QY 173 ELTTPVLPEETQEDAKKTFKESREAAALNLAY 204
Db 204 ELTTPVLPEETQEDAKKTFKESREAAALNLAY 235

RESULT 4
US-09-902-775A-137
; Sequence 137, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-137

Query Match 98.7%; Score 1092; DB 4; Length 382;
Best Local Similarity 96.2%; Pred. No. 5.5e-106;
Matches 204; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 GRLLS-----GQVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 52
Db 24 GRLLSASDLDLRGGQPCVCRGGTQPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIES 83

QY 53 EDEQKLIKFIENLLPSDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 112
Db 84 EDEQKLIKFIENLLPSDGFWIGLRRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEP 143

QY 113 SCGSEVCVVMYHQPAPAGIGGPFYMFQWNDRCNMKNNFICKYSDEKPAVPSREAEGET 172

Db 144 SCGSEVCVVMYHQPAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPAVPSREAEGET 203
QY 173 ELTTPVLPEETQEDAKKTFKESREAAALNLAY 204
Db 204 ELTTPVLPEETQEDAKKTFKESREAAALNLAY 235
RESULT 5
US-09-638-203-3
; Sequence 3, Application US/09638203
; Patent No. 6602501
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE
; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF
; FILE REFERENCE: 129.20USU1
; CURRENT APPLICATION NUMBER: US/09/638,203
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,935
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Hamster
US-09-638-203-3
Query Match 84.9%; Score 939.5; DB 4; Length 260;
Best Local Similarity 85.8%; Pred. No. 2.9e-90;
Matches 175; Conservative 9; Mismatches 19; Indels 1; Gaps 1;
QY 2 RLLSGQPVCRCGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI ESEDEQKLI EK 61
Db 1 RLLSGQLVCRGGTTRPCYKVIYFHDFAQRLNFEEAKEACRRDGGQLVSI ETEDEQRLIEK 60
QY 62 FIENLLPSDGFWIGLRRREEKQSNSTACQDLYAWTDGSI S QFRNWWYVDEPSCGSEVCV 121
Db 61 FIENLLASDGFWIGLRLRVKQVNTACQDLYAWTDGSI S QFRNWWYVDEPSCGSEVCV 120
QY 122 MYHQPAPAGIGGPFYMFQWDDRCNMKNFICKYSDEKPA -VPSREAEGETELTTPVLP 180
Db 121 MYHQPAPPGIGGPFYMFQWDDRCNMKNFICKYADEKPSITTPSRPGGEATEPTTPVLP 180
QY 181 EETQEDAKKTFKESREAAALNLAY 204
Db 181 EETQEDTKETFKESREAAALNLAY 204
RESULT 6
US-09-638-203-2
; Sequence 2, Application US/09638203
; Patent No. 6602501
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE
; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF
; FILE REFERENCE: 129.20USU1
; CURRENT APPLICATION NUMBER: US/09/638,203
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,935
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 273

; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-638-203-2
Query Match 50.8%; Score 561.5; DB 4; Length 273;
Best Local Similarity 60.1%; Pred. No. 1.1e-50;
Matches 101; Conservative 25; Mismatches 35; Indels 7; Gaps 3;
QY 2 RLLSGQPVCRCGTQPCYKVIYFHDTSRLNFEEAKEACRRDGGQLVSI ESEDEQKLI EK 61
Db 23 RVVSGQKVCFAADFKHPCYKMAVYFHELSSRVSFQEARLACEGGLVLSLENAEQKLIES 82
QY 62 FIENLLP-----SDGDFWIGLRRREEKQSNSTACQDLYAWTDGSI S QFRNWWYVDEPSCGS 116
Db 83 MLQNLTKPGTGISDGFWIGLWRNGDGT-SGACPDLYQWSDGSGNSQYRNWYTTDEPSCGS 141
QY 117 EVCVVMYHQPAPAGIGGPFYMFQWDDRCNMKNFICKYSDB-KPAVP 163
Db 142 EKCVMYHQPAPTANPGLGGPYLYQWDDRCNMKNHNYICKYEPINPTAP 189
RESULT 7
US-09-489-847-325
; Sequence 325, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 325
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-325
Query Match 20.9%; Score 231; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 8.2e-17;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GRLLSGQPVCRCGTQPCYKVIYFHDTSRLNFEEAKEACRR 42
Db 24 GRLLSGQPVCRCGTQPCYKVIYFHDTSRLNFEEAKEACRR 65
RESULT 8
US-09-489-847-234
; Sequence 234, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657

; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (82)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-234

Query Match 20.9%; Score 231; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 8.4e-17;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRLLSGQPVCRCGGTQRCYKVIYFHDTSRRLNFEEAKEACRR 42
Db 24 GRLLSGQPVCRCGGTQRCYKVIYFHDTSRRLNFEEAKEACRR 65

RESULT 9
US-09-489-847-324
; Sequence 324, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031PI
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 324
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-324

Query Match 20.9%; Score 231; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRLLSGQPVCRCGGTQRCYKVIYFHDTSRRLNFEEAKEACRR 42
Db 58 GRLLSGQPVCRCGGTQRCYKVIYFHDTSRRLNFEEAKEACRR 99

RESULT 10
US-09-976-594-168
; Sequence 168, Application US/09976594
; Patent No. 6673549

; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 168
; LENGTH: 1456
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 1674368CD1
US-09-976-594-168

Query Match 16.5%; Score 182; DB 4; Length 1456;
Best Local Similarity 25.5%; Pred. No. 5.6e-10;
Matches 52; Conservative 37; Mismatches 61; Indels 54; Gaps 8;
QY 19 YKVIYFHDTSRRLNFEEAKEACRRDGGQLVSIESDEQKLIKFIENLLPSDGFWIGLR 78
Db 807 YXDYYFYSKEKETMDNARAFCKRNFGLVSIQSEKKFLWKYV-NRNDAAQSAFYIGLL 865
QY 79 RREEKQSNSTACQDLVAVTDGSGISQFRNWYVDEPSCS--EVCVVMYHQPSAPAGIGGPY 136
Db 866 ISLDKK-----FAMDCSKVDYVSWATGEPNFEANEDENCVTMY-----SNSGF---- 908
QY 137 MFOWDDRCNMKNFNICKYSDEK----PAVPSREAEGETELTTPVLPEETQE----- 185
Db 909 ---WNDINCGYPNAFICQRHNSINATTVM-----TMPSPVSGCKEGWNFYSN 954
QY 186 -----EDAKTKFESREAAAL 200
Db 955 KCFKIFGFMEERKKNWQEARACI 978

RESULT 11
US-08-840-062-5
; Sequence 5, Application US/08840062
; Patent No. 6117977
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: WU, KAI
; TITLE OF INVENTION: TYPE C LECTINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,062
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1019R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881

TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-840-062-5

Query Match 16.1%; Score 178.5; DB 3; Length 1455;
Best Local Similarity 25.9%; Pred. No. 1.3e-09;
Matches 53; Conservative 33; Mismatches 66; Indels 53; Gaps 8;

QY 19 YKVIYFHTSRRLNFEAEACRRDGGQLVSISEDEQKLEKFIENLLPSDGFWIGLR 78
Db 806 YKDYQYFSEKETMDNARRFCNFGDLATIKSESEKFLWKYI-NKNGGQSPYFIGML 864
QY 79 RREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPSCGS--EVCVVMYHQPSAPAGIGGPY 136
Db 865 ISMDKK-----FIWMDGSKVDFVAWATGEPNFANDDENCVTMY-----TNSGF----- 907
QY 137 MFQWDDRCNMKNPFICK---YSDEKPAVPSREAEGEETELTPVLPETQEE----- 185
Db 908 ---WNDINCYPNNFICQHNSSINATAMP-----TTPTFGCKEGWHLYKVK 953
QY 186 -----EDAKTKFKESREAALNL 202
Db 954 CFKIFGFANEKKSWQDARQACKGL 978

RESULT 12
US-08-840-062-4
Sequence 4, Application US/08840062
Patent No. 611797
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: WU, KAI
TITLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,062
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1019R1
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1479 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-840-062-4

Query Match 16.0%; Score 176.5; DB 3; Length 1479;
Best Local Similarity 30.4%; Pred. No. 2.1e-09;
Matches 51; Conservative 25; Mismatches 57; Indels 35; Gaps 7;

QY 5 SGQPVCRGTQPCYKVIYFHTSRRLNFEAEACRRDGGQLVSISEDEQKLEKFIENLLPSDGFWIGLR 64
Db 385 SWQPF-----QGHCYRL-----QAEKRSWQESKKACLRGGGLVSIHSMAELEFITKQIK 434
QY 65 NLLPSDGFWIGLRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS---CGSEVCVV 121
Db 435 QEVE---ELWIGL-----NDLKLQMNFEWSGSLVSTFWHPFEPNFRDSDLEDCVT 483
QY 122 MYHQPSAPAGIGGPYMFQWDDRCNMKNPFICKYSDEKPAVPSREAEG 169
Db 484 IW---GPEG-----RWNDSPCNOQLPSICKKAGQLSQGAEEHDHG 520

RESULT 13
US-08-340-428B-49
Sequence 49, Application US/08340428B
Patent No. 5648465
GENERAL INFORMATION:
APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe
APPLICANT: MARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,428B
FILING DATE: 14 No. 5648465ember 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: Margolis-la
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-340-428B-49

Query Match 15.7%; Score 174; DB 1; Length 1257;
Best Local Similarity 30.8%; Pred. No. 3.1e-09;
Matches 44; Conservative 18; Mismatches 49; Indels 32; Gaps 6;

QY 15 QRPCYKVIYFHTSRRLNFEAEACRRDGGQLVSISEDEQKLEKFIENLLPSDGFW 74
Db 1037 QGHCYR--YF---AHRRAWEDAERDCRRRAGHLTSVHSPEEHKFINSF-----GHENSW 1085
QY 75 IGLRRREEKQSNSTACQDLYAWTDGSIQFRNWWYVDEPS---CGSEVCVVYHQPSAPAG 131
Db 1086 IGLNDRTVRD-----FQWTDNTGLQYENWREKQPDNFFAGGEDCVVMVAHENG--- 1134
QY 132 IGGPYMFQWDDRCNMKNPFICK 154

```

Db          1135 -----RWNDVPCNYNLPYVCK 1150      :||| ||| :|||
RESULT 14
5180808-2
;PATENT NO. 5180808
;APPLICANT: RUOSLAHTI, ERKKI I.
;TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN
;ANTIBODIES, AND METHODS OF DETECTING THE SAME
;NUMBER OF SEQUENCES: 4
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/441,179
;FILING DATE: 27-NOV-1989
;SEQ ID NO:2
;LENGTH: 2409
5180808-2
Query Match      15.7%; Score 174; DB 6; Length 2409;
Best Local Similarity 28.5%; Pred. No. 7.6e-09;
Matches 47; Conservative 23; Mismatches 55; Indels 40; Gaps 8;

Qy    15 QRPCYKVIYFHDTSRRLLNFEEAKEACRRDGGQLVSIESEDEQKLIEKFLENLPSDDGF - 73
       ||| ||| : | :: | | : || | | : | : | :
Db    2190 QGQCYS--YF---AHRRTWDAARECLRQGAHLTSLSHEEQMFVNRY-----GHDYQ 2237

Qy    74 WIGLRREEKGQNSTACQDLIAWTDGSIQFRNWYVDPEP----SCGSEVCVMVHQPSAP 129
       |||   : | :: | | : || | | : | : | : | : | :
Db    2238 WIGL-----NDKMFEHDFRWTGDSTLTQYENWRPNQPDSFFSAGEDCVVIIWHENG-- 2287

Qy    130 AGIGGPYMFQMNDRCNMKNFNICKYS-----DEKPVPFSREAEGE 170
       ||| ||| : | :: | | : || | | : | : | :
Db    2288 -----OWNDVPCNYHLTCTCKKGTIVACGQQPPVYENAKTFGK 2323

```

RESULT 15
US-08-840-062-2
; Sequence 2, Application US/08840062
; Patent No. 6117977
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: WU, KAI
; TITLE OF INVENTION: TYPE C LECTINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,062
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1019R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1479 amino acids
; TYPE: Amino Acid

[illegible]

	Query Match	13.7%;	Score 152;	DB 5;	Length 912;
	Best Local Similarity	28.8%;	Pred. No. 4.1e-07;		
	Matches	47;	Conservative	17;	Mismatches 61;
				Indels	38;
				Gaps	8;
QY	15	QRPCYKVIYFHDTSRRLLNFEEBAKEACRRDGGQLVSI	EESEDEQKLTIEKF	ENLLPSD	GDFW 74
Db	697	QGACYK----	HFSARR-SWEEAENKCRMYGAHLASISTPEEQDFINNRYREYQ-----	W	745
QY	75	IGLRRREEKQSNSTACQDLYAWTDGSI	SQFRNWWYDEPS---	CGSEVCVVM-YHQPS	A 130
Db	746	IGL-----	NDRTIEGDFLWSDGVPLLYENWNPGQPSYFLSGENCVVMVWH	DQ---	794
QY	131	GIGGPYMFQWDDRCNMKNNFICKYS-----	DEKPAVPSRE	AEG	169
Db	795	-----	QWSDVPCNYHLSTCKMGLVSCGPPPELPLAEVFG		829

RESULT 17
US-09-602-877A-99
; Sequence 99, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602.877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-602-877A-99

Query Match 13.7%; Score 151; DB 4; Length 197;
Best Local Similarity 25.0%; Pred. No. 6.5e-08;
Matches 38; Conservative 26; Mismatches 64; Indels 24; Gaps 4;
QY 7 QPVCRRGGTQ--RPGYKVIYFHDTSRRRLNFEEAKEACRRDGGQLVSIIESEDEQKLIKPFIE 64
Db 65 QTVCLRGTKVHKCYLA-----SEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGK 119
QY 65 NLLPSDGDFFWGLRRREEKQSNSTACQDLYAWTDGSIQFRNMYVDEPSCGSEVGVVYH 124
Db 120 RSLPGVNDFWLGI-----NDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFS 171
QY 125 QPSAPAGIGGPFYMFQWDDRCNMKNFICKYS 156
Db 172 QSA-----QKWSDEACRSSKRYICEFT 194

RESULT 18
US-09-866-028-50
; Sequence 50, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866.028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 50
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-50

Query Match 13.5%; Score 149.5; DB 4; Length 455;
Best Local Similarity 25.6%; Pred. No. 2.9e-07;
Matches 45; Conservative 25; Mismatches 61; Indels 45; Gaps 8;
QY 12 GGTORPCYKVIY--FHDTSRRLN-----FEEAKEACRRDGGQLVSIIESEDEQK 57
Db 287 GGAQ--CATKVHFPFHTCDLRIDGCFMVSSSEADTYRARMKQCKGGLAQIKSQKVD 344
QY 58 LIEKFIENLLP-----SDGD-----FWIGLRRREEKQSNSTACQDLYAWTDGSIQFRNMY 108
Db 345 ILAFYLGRLTNEVTDSDFETRNFWIGLTYKTAK-----DSFRWATGEHQAFSTSA 396
QY 109 VDEPSCGSEVGVVYHQPSPAPAGIG-----GPYMFQWDDRCNMKNFICKYSDE 158
Db 397 FGQPDNHGLVWL-----SAAMGFGNCVELQASAAFNWDDRCNRYICQFAQE 446

RESULT 19
US-07-641-971B-1
; Sequence 1, Application US/07641971B
; Patent No. 5236706
; GENERAL INFORMATION:
; APPLICANT: Debre, Patrice
; APPLICANT: Mossalayi, Mohammed D
; TITLE OF INVENTION: A PHARMACEUTICAL PREPARATION FOR THE
; TITLE OF INVENTION: MATURATION OF PROTHYMOCYTES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation
; STREET: 556 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/641,971B
; FILING DATE: 19910116
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 90016254
; FILING DATE: 24-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fishman, Irving M
; REGISTRATION NUMBER: 30258
; REFERENCE/DOCKET NUMBER: 4-17921/+ /DEB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-277-4832
; TELEFAX: 908-277-4306
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; CELL TYPE: Human B. Cells
; CELL LINE: CHO cells transformed with pCAL8-BF-ND
US-07-641-971B-1

Query Match 13.5%; Score 149; DB 1; Length 174;
Best Local Similarity 30.2%; Pred. No. 8.9e-08;
Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;
QY 15 QRPCYKVIYFHDTSRRLNFEAKEACRRDGGQLVSIIESEDEQKLIKFIENLLPSDGD 74

Db 24 QKCY---YFGKGTQ--WVHARYACDDMEGQLVSIHSPPEQDFTLTKH-----ASHTGSW 73

QY 75 IGLRREEKQSNSTACQDLYAWTDGSIQFRNWNVYVDEPSCGS--EVCVVMYHQPSAPAGI 132

Db 74 IGLRNLDLKGE-----FIWVDGSHVDYSNWPAGEPTSRSQGEDCVMM-----RGS 118

QY 133 GGPYMFQWNDRCNMK--NNFICKYSDEKPAV---PSREAAGE-----ETELTPV 178

Db 119 G-----RWNDAFCDRKLGAWVC-----DRLATCTPPASEGSAESMGPDSPDPDGRLLPTPS 169

QY 179 LP 180

Db 170 AP 171

RESULT 20

US-07-781-248A-1

; Sequence 1, Application US/07781248A

; Patent No. 5246699

; GENERAL INFORMATION:

; APPLICANT: Debre, Patrice

; APPLICANT: Mossalayi, Mohammed D

; TITLE OF INVENTION: MATURATION OF HEMATOPOIETIC CELLS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation

; STREET: 556 Morris Avenue

; CITY: Summit

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07901

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0; Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07781,248A

; FILING DATE: 19911230

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 90103565

; FILING DATE: 09-MAY-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Ikeler, Barbara J.

; REGISTRATION NUMBER: 36,170

; REFERENCE/DOCKET NUMBER: 4-18065/A/DEB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908-277-3368

; TELEFAX: 908-277-4306

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 174 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; CELL TYPE: Human B. Cells

; CELL LINE: CHO cells transformed with pCAL8-BF-ND

US-07-781-248A-1

Query Match 13.5%; Score 149; DB 1; Length 174;

Best Local Similarity 30.2%; Pred. No. 8.9e-08;

Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

QY 15 QRPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIHSPPEQDFTLTKH-----ASHTGSW 74

Db 24 QKCY---YFGKGTQ--WVHARYACDDMEGQLVSIHSPPEQDFTLTKH-----ASHTGSW 73

QY 75 IGLRREEKQSNSTACQDLYAWTDGSIQFRNWNVYVDEPSCGS--EVCVVMYHQPSAPAGI 132

Db 74 IGLRNLDLKGE-----FIWVDGSHVDYSNWPAGEPTSRSQGEDCVMM-----RGS 118

QY 133 GGPYMFQWNDRCNMK--NNFICKYSDEKPAV---PSREAAGE-----ETELTPV 178

Db 119 G-----RWNDAFCDRKLGAWVC-----DRLATCTPPASEGSAESMGPDSPDPDGRLLPTPS 169

QY 179 LP 180

Db 170 AP 171

RESULT 21

US-08-365-103B-10

; Sequence 10, Application US/08365103B

; Patent No. 5766943

; GENERAL INFORMATION:

; APPLICANT: Lynch, Richard G

; APPLICANT: Nunez, Raphael D.

; APPLICANT: Yodoi, Jungi

; TITLE OF INVENTION: DNA Sequences for Soluble Proms of CD23

; TITLE OF INVENTION: and Methods of Use for Same

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease

; STREET: 801 Grand Ave. Suite 3200

; CITY: Des Moines

; STATE: Iowa

; COUNTRY: United States

; ZIP: 50309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0; Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/365,103B

; FILING DATE: 28-DEC-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Nebel, Heidi S.

; REGISTRATION NUMBER: 37,719

; REFERENCE/DOCKET NUMBER: Uirf N5-24

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (515) 288-3667

; TELEFAX: (515) 288-1338

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 320 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-365-103B-10

Query Match 13.5%; Score 149; DB 1; Length 320;

Best Local Similarity 30.2%; Pred. No. 2e-07;

Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

QY 15 QRPCYKVIYFHDTSRRLNFEBAKEACRRDGGQLVSIHSPPEQDFTLTKH-----ASHTGSW 74

Db 170 QKCY---YFGKGTQ--WVHARYACDDMEGQLVSIHSPPEQDFTLTKH-----ASHTGSW 219

QY 75 IGLRREEKQSNSTACQDLYAWTDGSIQFRNWNVYVDEPSCGS--EVCVVMYHQPSAPAGI 132

Db 220 IGLRNLDLKGE-----FIWVDGSHVDYSNWPAGEPTSRSQGEDCVMM-----RGS 264

QY 133 GGPYMFQWNDRCNMK--NNFICKYSDEKPAV---PSREAAGE-----ETELTPV 178

Db 265 G-----RWNDAFCDRKLGAWVC-----DRLATCTPPASEGSAESMGPDSPDPDGRLLPTPS 315

QY 179 LP 180

Db 316 AP 317

RESULT 22

US-08-365-103B-8

; Sequence 8, Application US/08365103B

; Patent No. 5766943

; GENERAL INFORMATION:

; APPLICANT: Lynch, Richard G

; APPLICANT: Nunez, Raphael D.

; APPLICANT: Yodoi, Junji

; TITLE OF INVENTION: DNA Sequences for Soluble Forms of CD23

; TITLE OF INVENTION: and Methods of Use for Same

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease

; STREET: 801 Grand Ave. Suite 3200

; CITY: Des Moines

; STATE: Iowa

; COUNTRY: United States

; ZIP: 50309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/365,103B

; FILING DATE: 28-DEC-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Nebel, Heidi S.

; REGISTRATION NUMBER: 37,719

; REFERENCE/DOCKET NUMBER: Uirf N5-24

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (515) 288-3667

; TELEFAX: (515) 288-1338

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 321 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-365-103B-8

Query Match 13.5%; Score 149; DB 1; Length 321;

Best Local Similarity 30.2%; Pred. No. 2e-07;

Matches 55; Conservative 20; Mismatches 57; Indels 50; Gaps 11;

QY 15 QRPCYKVIYFHDTSRLNFEAEKACERDGGQLVSIKIEKFIENLLPSDGF 74

Db 171 QKCY---YFGKGTQ--WVHARYACDDMEGQLVSIHSPEDQFLTKH-----ASHTGSW 220

QY 75 IGLRRREKQSNSTACQDLYAWTDGSIQSRNWNVYVDEPSCGS--EVCVMYHQSAPAGI 132

Db 221 IGLRNLKGE-----FIWVDGSHVDYSNWAPGEPTRSQGEDCVMM-----RGS 265

QY 133 GGPYMFQWDDRCNMK--NNFICKISDEKPAV---PSRAEGE-----ETELTTPV 178

Db 266 G-----RWDAFCDRKLGAWVC-----DRLATCTPPASEGSAESMGPSRPPDGRLP 316

QY 179 LP 180

Db 317 AP 318

RESULT 23

US-08-751-305-2

; Sequence 2, Application US/08751305

; Patent No. 5965439

; GENERAL INFORMATION:

; APPLICANT: Tenner et al., Andrea J.

; TITLE OF INVENTION: HOST DEFENSE ENHANCEMENT

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/751,305

; FILING DATE: 18-NOV-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Wetherell, Jr., John R.

; REGISTRATION NUMBER: 31,678

; REFERENCE/DOCKET NUMBER: 07306/012001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 652 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-751-305-2

Query Match 13.4%; Score 148.5; DB 2; Length 652;

Best Local Similarity 24.4%; Pred. No. 6e-07;

Matches 50; Conservative 37; Mismatches 75; Indels 43; Gaps 9;

QY 3 LLSGQP-----VCRGGTQPCYKVIYFHDTSRLNFEAEKACRRDGGQLVSI 51

Db 13 LLLTQPGAGTGADTEAVCVG---TACYTA-----HSGKLSAAEAQHCNONGNLATVK 64

QY 52 SEDEQKLIKFIENLLPSD-----GDFWIGLRRRREKQSNSTACQDLYAWT-DGSISQ 103

Db 65 SKEEAQHVRVLAQLLRREAALTARMSKFWIGLQREKKGKCLDPSLPLKGFVWVGGEDTP 124

QY 104 FRNWTVD-EFSCGSEVCVVM---YHQPAPAGIGGYPYMFQWDDRCNMKN-----FI 152

Db 125 YSNWHKELRNSCISKRCVSLLLDLSQPLLPNRLP-----KWSEGPCGSPGSPGSGNIEGFV 179

QY 153 KYSDEKPAVPSRAEGEETELTTP 177

Db 180 CKFSFKGMCRLALGGPGQVTVTTP 204

RESULT 24

US-09-517-605-2

; Sequence 2, Application US/09517605

; Patent No. 6391567

; GENERAL INFORMATION:

; APPLICANT: Littman, Dan R.

; APPLICANT: Kwon, Douglas S.

; APPLICANT: van Kooyk, Yvette

; APPLICANT: Geijtenbeck, Theo

; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO

; TITLE OF INVENTION: CELLS

; FILE REFERENCE: 1049-1-017

; CURRENT APPLICATION NUMBER: US/09/517,605

; CURRENT FILING DATE: 2000-03-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Homo sapiens

Query Match	13.0%;	Score 143.5;	DB 2;	Length 372;
Best Local Similarity	26.5%;	Pred. No. 9.3e-07;		
Matches 41;	Conservative 37;	Mismatches 50;	Indels 27;	Gaps 8;

Search completed: September 9, 2004, 22:58:15
Job time : 17.0393 secs

Query Match	13.0%;	Score 143.5;	DB 2;	Length 372;
Best Local Similarity	26.5%;	Pred. No. 9.3e-07;		
Matches 41;	Conservative 37;	Mismatches 50;	Indels 27;	Gaps 8;

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